

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 21:30:19 ; Search time 2563.57 Seconds
(without alignments)
17175.023 Million cell updates/sec

Title: US-08-908-884-2

Perfect score: 2104
Sequence: 1 TCGATCTTTACCAATCCA.....ATAAAAAAAAAAAAAAAAAA 2104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463260293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl :

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_ma:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
------------	-------	-------	-------	--------	----	-------------

1	2104	100.0	2104	8	ATU76707	U76707 Arabidopsis
2	2083.8	99.0	2154	8	AY050455	AY050455 Arabidopsis
3	2009.4	95.5	2011	6	AR087502	AR087502 Sequence
4	2006.2	95.4	2011	6	AR087503	AR087503 Sequence
5	1761	83.7	96887	8	AC066689	AC066689 Arabidopsis
6	1760	83.7	5655	8	AR087501	AR087501 Sequence
7	1760	83.7	5655	8	ATU87794	U87794 Arabidopsis
8	1605	76.3	1608	6	AR087505	AR087505 Sequence
9	1592.8	75.7	1597	6	AR087504	AR087504 Sequence
10	1188.4	56.5	1194	6	AR087506	AR087506 Sequence
11	781.4	37.1	786	6	AR087507	AR087507 Sequence
12	686.4	32.6	104738	8	ATF20B18	AL049483 Arabidopsis
13	686.4	32.6	196286	8	ATCHRIV64	AL161564 Arabidopsis
14	360.4	17.1	1565	6	AX351141	AX351141 Sequence
15	314.6	15.0	1668	6	AX351145	AX351145 Sequence
16	260.2	12.4	2368	6	AX049427	AX049427 Sequence
17	259.4	12.3	140304	8	AP002537	AP002537 Oryza sat
18	259.4	12.3	168372	8	AP002746	AP002746 Oryza sat
19	258.6	12.3	1428	6	AX049426	AX049426 Sequence
20	258.6	12.3	2326	6	AX351139	AX351139 Sequence
21	241.6	11.5	4270	6	AX351127	AX351127 Sequence
22	232.6	11.1	2154	6	AX041006	AX041006 Sequence
23	200.4	9.5	1830	6	AX049431	AX049431 Sequence
24	200.4	9.5	2120	6	AX049433	AX049433 Sequence
25	199.4	9.5	498	6	AX351135	AX351135 Sequence
26	196.8	9.4	2446	6	AX351143	AX351143 Sequence
27	195.2	9.3	1824	6	AX049430	AX049430 Sequence
28	195.2	9.3	2420	6	AX049432	AX049432 Sequence
29	194.2	9.2	1385	6	AX049441	AX049441 Sequence
30	192.6	9.2	2235	6	AX049445	AX049445 Sequence
31	186.8	8.9	705	6	AX049428	AX049428 Sequence
32	170.2	8.1	498	6	AX351133	AX351133 Sequence
33	169.6	8.1	103785	2	AP003377	AP003377 Oryza sat
34	169.6	8.1	140823	2	AP003371	AP003371 Oryza sat
35	159.2	7.6	67720	8	AB019224	AB019224 Arabidopsis
36	153	7.3	7789	6	AX041008	AX041008 Sequence
37	145.4	6.9	706	6	AX049434	AX049434 Sequence
38	142.2	6.8	95417	8	ATT16H5	AL024486 Arabidopsis
39	142.2	6.8	197114	8	ATCHRIV51	AL161551 Arabidopsis
40	138.6	6.6	498	6	AX351137	AX351137 Sequence
41	69	3.3	77923	8	AC064840	AC064840 Arabidopsis
42	69	3.3	102135	8	AC069144	AC069144 Arabidopsis
43	64	3.0	2013	8	AF419581	AF419581 Arabidopsis
44	54.2	2.6	91303	8	ATF24I3	AL138655 Arabidopsis
45	51.6	2.5	110000	2	PFMAL13P2_0	AL049185 Plasmodiu

ALIGNMENTS

RESULT 1	ATU76707	Arabidopsis thaliana	2104 bp	linear	PLN 13-JAN-1997
LOCUS	ATU76707	Arabidopsis thaliana	cds	mrna	NPRI (NPRI) mRNA, complete
DEFINITION	ATU76707	Arabidopsis thaliana	cds		
ACCESSION	U76707	U76707.1	GI:1773294		
VERSION	U76707				
KEYWORDS	U76707				
SOURCE	U76707	thale cress.			
ORGANISM	U76707	Arabidopsis thaliana			
REFERENCE	U76707	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	U76707	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
TITLE	U76707	Rosidae; eurosids ii; Brassicales; Brassicaceae; Arabidopsis.			
JOURNAL	U76707	1 (bases 1 to 2104)			
MEDLINE	U76707	Cao,H., Glazebrook,J., Clarke,J.D., Volko,S. and Dong,X.			
REFERENCE	U76707	The Arabidopsis NPRI gene that controls systemic acquired			
AUTHORS	U76707	resistance encodes a novel protein containing ankyrin repeats			
TITLE	U76707	Cell 88 (1), 57-63 (1997)			
JOURNAL	U76707	97148688			
MEDLINE	U76707	2 (bases 1 to 2104)			
REFERENCE	U76707	Cao,H., Glazebrook,J., Clarke,J.D., Volko,S. and Dong,X.			
AUTHORS	U76707	Direct Submission			
TITLE	U76707	Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC			
JOURNAL	U76707				

Building, Research Dr., Durham, NC 27708-1000, USA

FEATURES

source
1..2104
/organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
/chromosome="1"
/map="between GAP-B and m315"
1..2104
/gene="NP1"
93..1874
/gene="NP1"
/note="ankyrin repeat-containing protein; gene controlling systemic acquired resistance; SAR"
/codon_start=1
/product="regulatory protein NP1"
/protein_id="AAC49611.1"
/db_xref="gi:1773295"
/translation="MDTIDGFADSYEISSTSFVATDNTDSSIVYLAEOVLTPDVS
ALQLLSFESFSDPDDFYSDAKLVLDSDREVSHRCVLSARSPFKSALAARKKEK
DSNNTAAVKLEKEIAKDYEVGDSVTVLAIYVSSRVPPKGVSECADENCHVAC
RPAYDFLEVLIAFIKIPELITLYQRIHLLVVDVVKVYIEDTILVILKANICRACMK
LDRCKEILVKNVDMVSLKSLPEELVKEIIDRRKELGLEVPKVKHVNINAKALDS
DDIELVLLKEDHTDDACALHFAYCNVKTATDLKLDLADVNHRNPRTYVILH
VAAMEKPOLILSLLEGASAEATLEGRALMIKATWAVECNNTPEOCKSLKGR
LCVELBEQDREQIPRDVPSFAVADELKMTLLDLENRVALAORLPTFEAQAAMEI
AEMKGTCEFIYVTSLEPRLTGTKRTSFGVKATLPERILLEHQSRKLKSLKTVELGKRF
PRCSAVLDQIMNCEDLTLQACGEDDTAEKRLQKQRYWEIQETILKKAISEDNLGNS
SLTDSSTSKSTGCKSRNKLSHRRR"
BASE COUNT 606 a 431 c 482 g 585 t
ORIGIN

Query Match 100.08; Score 2104; DB 8; Length 2104;
Best Local Similarity 100.08; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCATCTTTAAACCAATCCAGTTGATAAGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60
DB 1 TCATCTTTAAACCAATCCAGTTGATAAGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60
QY 61 ATTTGTGAATTCATTCGGAACCTCTTGATGACACACCATTTGATGATTCGCGG 120
DB 61 ATTTGTGAATTCATTCGGAACCTCTTGATGACACACCATTTGATGATTCGCGG 120
QY 121 ATTCCTATGAATACAGCAGACTAGTTTCGTCGCTACCCGATTAACACGACTCCTATTG 180
DB 121 ATTCCTATGAATACAGCAGACTAGTTTCGTCGCTACCCGATTAACACGACTCCTATTG 180
QY 181 TTTATCTGCGCGCGGCAACAGTACTCACCGACCTGATGATCTGCTGCAATTGCTCT 240
DB 181 TTTATCTGCGCGCGGCAACAGTACTCACCGACCTGATGATCTGCTGCAATTGCTCT 240
QY 241 CCAACAGCTTCGAATCCGCTTTGACTCGCGGATGATTTACAGCGACGCTAAGCTTG 300
DB 241 CCAACAGCTTCGAATCCGCTTTGACTCGCGGATGATTTACAGCGACGCTAAGCTTG 300
QY 301 TTCTCTCCGACGCGCGGGAAGTTTCTTCCACCGGTGCGTTTGTTCAGCGAGAAGCTCT 360
DB 301 TTCTCTCCGACGCGCGGGAAGTTTCTTCCACCGGTGCGTTTGTTCAGCGAGAAGCTCT 360
QY 361 TCTTCAAGACGCTTTAGCGCGCGCTTAAGNAGAGAAAGACTCCACACACCGCGCGG 420
DB 361 TCTTCAAGACGCTTTAGCGCGCGCTTAAGNAGAGAAAGACTCCACACACCGCGCGG 420
QY 421 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGGTTTGTGA 480
DB 421 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGGTTTGTGA 480
QY 481 CTGTTTTGGCTTAFTGTTTACAGCAGCAGAGTGAACCGCGCCCTAAAGGAGTTTCTGAAT 540
DB 481 CTGTTTTGGCTTAFTGTTTACAGCAGCAGAGTGAACCGCGCCCTAAAGGAGTTTCTGAAT 540
QY 541 GCGCAGACGAGAAATTCGTCGCACGTGGCTTGC CGCGCGCGGGTTCATGTTGGAGG 600

DB 541 GCGCAGACGAGAAATTCGTCGCACGTGGCTTGC CGCGCGCGGGTTCATGTTGGAGG 600
QY 601 TTCTCTATTTGGCTTTTCATCTTCAAGATCCCTGCAATTAATCTCTCTATCAGAGCACT 660
DB 601 TTCTCTATTTGGCTTTTCATCTTCAAGATCCCTGCAATTAATCTCTCTATCAGAGCACT 660
QY 661 TATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTATCTCAAGCTTGCTA 720
DB 661 TATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTATCTCAAGCTTGCTA 720
QY 721 ATATATGTGTTAAAGCTTGTATGAAGCTATTTGGATAGATGTAAGAGATTTATGTCAGT 780
DB 721 ATATATGTGTTAAAGCTTGTATGAAGCTATTTGGATAGATGTAAGAGATTTATGTCAGT 780
QY 781 CTATATGTAGATATGTTAGTCTTTGAAAAGTCATTGCCGGAAGAGCTTGTGTTAAAGAGATAA 840
DB 781 CTATATGTAGATATGTTAGTCTTTGAAAAGTCATTGCCGGAAGAGCTTGTGTTAAAGAGATAA 840
QY 841 TTGATAGACCTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACATGTCGCAATG 900
DB 841 TTGATAGACCTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACATGTCGCAATG 900
QY 901 TACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTCAAGAGAGATC 960
DB 901 TACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTCAAGAGAGATC 960
QY 961 ACACCAATCTAGATGATGCGTGTCTCTTCAATTCGCTGTTGTCATATTGCAATGTTGAAGA 1020
DB 961 ACACCAATCTAGATGATGCGTGTCTCTTCAATTCGCTGTTGTCATATTGCAATGTTGAAGA 1020
QY 1021 CCGCAACAGATCTTTTAAAACTTGATCTTCGCGATGTCACCATAGGAATCCGAGGGAT 1080
DB 1021 CCGCAACAGATCTTTTAAAACTTGATCTTCGCGATGTCACCATAGGAATCCGAGGGAT 1080
QY 1081 ATACGGTGTCTTATGTTGCTCGGATCGGAAGGACACCAATTTGATACTATCTCTATTGG 1140
DB 1081 ATACGGTGTCTTATGTTGCTCGGATCGGAAGGACACCAATTTGATACTATCTCTATTGG 1140
QY 1141 AAAAAGTGCAGTGCATCAGAAGCAACTTTTGAAGGTAGAAGCGCACTCATGATCGCAA 1200
DB 1141 AAAAAGTGCAGTGCATCAGAAGCAACTTTTGAAGGTAGAAGCGCACTCATGATCGCAA 1200
QY 1201 AACAGGCACATATGGCGGTTGAATGTAATATATCCCGGAGCAATCAAGCAATTTCTCTCA 1260
DB 1201 AACAGGCACATATGGCGGTTGAATGTAATATATCCCGGAGCAATCAAGCAATTTCTCTCA 1260
QY 1261 AAGCGGCACTATGTAGAAATCTAGAGCAAGAGACAAACAGAGAAATTCCTTAGAG 1320
DB 1261 AAGCGGCACTATGTAGAAATCTAGAGCAAGAGACAAACAGAGAAATTCCTTAGAG 1320
QY 1321 ATGTTCTCCCTCTTTTTCAGTGGCGCGGATGAATTTGAAGATGACGCTGCTCATCTTG 1380
DB 1321 ATGTTCTCCCTCTTTTTCAGTGGCGCGGATGAATTTGAAGATGACGCTGCTCATCTTG 1380
QY 1381 AAAATAGAGTTGCACTTCTCAAGCTCTTTTCCAAAGGAGAGACAAAGCTGCAATGGAGA 1440
DB 1381 AAAATAGAGTTGCACTTCTCAAGCTCTTTTCCAAAGGAGAGACAAAGCTGCAATGGAGA 1440
QY 1441 TCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCTGAGCTGACGCTCTCA 1500
DB 1441 TCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCTGAGCTGACGCTCTCA 1500
QY 1501 CTGGTACGAAGAGACATCACCGGTTGTAAGATAGCACTTTCCAGATCTCTAGAAGAGC 1560
DB 1501 CTGGTACGAAGAGACATCACCGGTTGTAAGATAGCACTTTCCAGATCTCTAGAAGAGC 1560
QY 1561 ATCAAGTAGACTAAAGCGCTTTCTAAAAACCGTGGAACTCGGGAACGATTTCTCCCGC 1620
DB 1561 ATCAAGTAGACTAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGATTTCTCCCGC 1620
QY 1621 GCTGTGCGCAGTGTGCGACCAAGATTTGAACTGTGAGACTTGACTCAACTGCTGCTGCG 1680

```
Db 1621 GCTGTTCCGCGAGTCTCGACGAGATTATGAACCTGTGAGGACTTGACTCAACTGCCTTGGC 1680
QY 1681 GAGAAGACGACACTGCTGAGAAAGCACTACAAAGAGCAAGGACGATCATGGAATACAAG 1740
Db 1681 GAGAGACGACACTGCTGAGAAAGCACTACAAAGAGCAAGGACGATCATGGAATACAAG 1740
QY 1741 AGACACTAAAGAAGCGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTCGTCCTCGACAG 1800
Db 1741 AGACACTAAAGAAGCGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTCGTCCTCGACAG 1800
QY 1801 ATTGCACTCTTCCACATCAAAATCAACCGTGGAAGAGGCTTAACCGTAAACTCTCTC 1860
Db 1801 ATTGCACTCTTCCACATCAAAATCAACCGTGGAAGAGGCTTAACCGTAAACTCTCTC 1860
QY 1861 ATCGTCGTCGGTGAGACTCTTGCTCTTCTAGTGAATTTTGTGTTGACCATATAATTTCTGT 1920
Db 1861 ATCGTCGTCGGTGAGACTCTTGCTCTTCTAGTGAATTTTGTGTTGACCATATAATTTCTGT 1920
QY 1921 TTTTCATGATGACGTGAACCTGTTTATGCTATCCTATGCTGTCGCTCATATATAGTTTCGCTCTTCGT 1980
Db 1921 TTTTCATGATGACGTGAACCTGTTTATGCTATCCTATGCTGTCGCTCATATATAGTTTCGCTCTTCGT 1980
QY 1981 TTTGCACTCTGTTATATTTGCTGAGGCTGCTTCAACAAATGTTGTAACAATTTGAA 2040
Db 1981 TTTGCACTCTGTTATATTTGCTGAGGCTGCTTCAACAAATGTTGTAACAATTTGAA 2040
QY 2041 CCAATGTTATACAGATTTGTAATATATATTTATGTCATCAACAATAAAAAA 2100
Db 2041 CCAATGTTATACAGATTTGTAATATATATTTATGTCATCAACAATAAAAAA 2100
QY 2101 AAAA 2104
Db 2101 AAAA 2104

RESULT 2
AY050455
LOCUS
DEFINITION
Arabidopsis thaliana Atlg64280/F15H21_6 mRNA, complete cds.
ACCESSION
AY050455
VERSION
AY050455.1 GI:15215849
KEYWORDS
F11_CDNA.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2154)
Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P.,
Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D.,
Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,
Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,
Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
Arabidopsis cDNA clones
Unpublished
2 (bases 1 to 2154)
Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P.,
Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D.,
Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A.,
Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,
Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J.,
Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
Direct Submission
Submitted (08-AUG-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
```

collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P., Banh,J., Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

Koesema,E. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

source	location/Qualifiers
1..2154	
/organism="Arabidopsis thaliana"	
/db_xref="taxon:3702"	
/chromosome="1"	
/clones="RAFL07-16-K16(R13446)"	
/note="ecotype: Columbia"	
1..158	
159..1940	
/note="transcription factor inhibitor I kappa B, putative"	
/codon_start=1	
/product="Atlg64280/F15H21_6"	
/protein_id="AAK91469.1"	
/db_xref="GI:15215850"	
/translation="MDTIDGFADSYEISSTFVATDNTDSSIVYLAEEVLPDVS ALQLSNSFVDPDFYSDAKLVLDGSEVFRHCVLSARSSFFKSALAARKKEK DSNNTAAVKLELAFIAKIDYEGFDSVTVLAYVYSSVRPPKPGSECDNCCHVAC RPADFMLEYLAFIKIPDLITLYQHLLDVVKVIIEDTLVLKLANICGACWK LDRCKEIIVKSNVDMVSLKPSLPEELVKEIIDRKLGLVLPVKHVSNNVKHALDS DDEIKVLLKEDHTNLDACALHVAVCNVKATDLDLADLVNHNPRGYTVLH VAMKEPOLILSLEKASASEATLEGRTALMIAKOATWAVECNINPEOCKSLKGR LCVEILQEDKROIROPDVPFSAVADELKMTLLDLENVALAQLRFLPTEAQAAMEI AEMKGTCEFIIVTSLEPRLTGTGRTSPGVAPIFRILEHQSRLKSLSKTVEIGKRF PRCSAVLDQIMNGEDDTQLACGEDDTAEKRLQKKQRYMEIQETLKKAFSDNLELNS SLTDSSTSKSTGCKRSNRKLSHRRR"	
1941..2154	
BASE COUNT 602 a 450 c 493 g 609 t	
ORIGIN	
Query Match 99.0%; Score 2083.8; DB 8; Length 2154;	
Best Local Similarity 99.9%; Pred. No. 0;	
Matches 2085; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy 1 TCGATCTTTAACCAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60	
Db 67 TCGATCTTTAACCAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 126	
Qy 61 ATTTGTGAATTCGAATTCATCGGACCTGTTGATGGACACCACTTTCATGGATTCGCG 120	
Db 127 ATTTGTGAATTCGAATTCATCGGACCTGTTGATGGACACCACTTTCATGGATTCGCG 186	
Qy 121 ATTCCTATGAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCTCTATTG 180	
Db 187 ATTCCTATGAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCTCTATTG 246	
Qy 181 TTTATCTGGCGCGGACAAAGTACTACCGGACCTGATGATATCTGCTCTCAATTCGCT 240	
Db 247 TTTATCTGGCGCGGACAAAGTACTACCGGACCTGATGATATCTGCTCTCAATTCGCT 306	
Qy 241 CCAACAGCTTCGAATTCGCTCTTTCGTCGCGGATGATTTCTACAGCAGCCTTAAGCTTG 300	
Db 307 CCAACAGCTTCGAATTCGCTCTTTCGTCGCGGATGATTTCTACAGCAGCCTTAAGCTTG 366	
Qy 301 TTCTCTCCGCGCGGGAAGTTCTTTTCCACCGTGCCTTTTTCAGCGAAGAGCTCTT 360	
Db 367 TTCTCTCCGCGCGGGAAGTTCTTTTCCACCGTGCCTTTTTCAGCGAAGAGCTCTT 426	

```
QY 361 TCCTCAAGAGCGCTTTAGCGCGCTTAAGAGGAGAAAGACTCCAACAACACCGCGCGC 420
Db 427 TCCTCAAGAGCGCTTTAGCGCGCTTAAGAGGAGAAAGACTCCAACAACACCGCGCGC 486
QY 421 TGAAGCTCAGAGCTTAAGAGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGGA 480
Db 487 TGAAGCTCAGAGCTTAAGAGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGGA 546
QY 481 CTGTTTGGCTTATGTTTACAGCAGCAGAGTCAGACCGCGCCCTTAAGAGCTTCTGAAT 540
Db 547 CTGTTTGGCTTATGTTTACAGCAGCAGAGTCAGACCGCGCCCTTAAGAGCTTCTGAAT 606
QY 541 GCGCAGCAGAGAAATGCTGCCACGTCGGTTGCGCGCGCGCGCTGGAATTCATGTTGAGG 600
Db 607 GCGCAGCAGAGAAATGCTGCCACGTCGGTTGCGCGCGCGCGCTGGAATTCATGTTGAGG 666
QY 601 TTCCTCAATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTATCAGAGGCACT 660
Db 667 TTCCTCAATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTATCAGAGGCACT 726
QY 661 TATTTGACGCTTCTAGACAAAGTTGTTATAGAGGACACATTTGGTTATCTCAAGCTTGCTA 720
Db 727 TATTTGACGCTTCTAGACAAAGTTGTTATAGAGGACACATTTGGTTATCTCAAGCTTGCTA 786
QY 721 ATATATGTTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGAGATTAATGTCAGT 780
Db 787 ATATATGTTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGAGATTAATGTCAGT 846
QY 781 CTAATGTAGATATGTTAGTCTTGAAGAGTCAATTCGCCGGAAGAGCTTGTAAAGAGATAA 840
Db 847 CTAATGTAGATATGTTAGTCTTGAAGAGTCAATTCGCCGGAAGAGCTTGTAAAGAGATAA 906
QY 841 TTGATAGAGCTTAAGAGCTTGTGTTGGAGTACCTAAAGTAAGAAACATGCTCGAATG 900
Db 907 TTGATAGAGCTTAAGAGCTTGTGTTGGAGTACCTAAAGTAAGAAACATGCTCGAATG 966
QY 901 TACATAAGCAGCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAGAGGATC 960
Db 967 TACATAAGCAGCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAGAGGATC 1026
QY 961 ACACCAATCTAGATAGTGGTGTCTTCATTTGCTGTTGCATATTGCAATGTCATGGAAGA 1020
Db 1027 ACACCAATCTAGATAGTGGTGTCTTCATTTGCTGTTGCATATTGCAATGTCATGGAAGA 1086
QY 1021 CCGCAACAGATCTTTAAACCTTGATCTTGGCGATGTCAACCATAGGAATCCGAGGGAT 1080
Db 1087 CCGCAACAGATCTTTAAACCTTGATCTTGGCGATGTCAACCATAGGAATCCGAGGGAT 1146
QY 1081 ATACGGTGTCTCATGTTGCTGCGATGCGGAAGGACCAATGTATCTCTATTG 1140
Db 1147 ATACGGTGTCTCATGTTGCTGCGATGCGGAAGGACCAATGTATCTCTATTG 1206
QY 1141 ARAAGGTCAGTGCATCAGAGCAACTTTTGAAGGTAGAACCGCACTCATGATCGCAA 1200
Db 1207 ARAAGGTCAGTGCATCAGAGCAACTTTTGAAGGTAGAACCGCACTCATGATCGCAA 1266
QY 1201 AACAAGCCACTATGCGGTTGAATGTAATATATCCCGAGCAATGCAAGCATTTCTCTCA 1260
Db 1267 AACAAGCCACTATGCGGTTGAATGTAATATATCCCGAGCAATGCAAGCATTTCTCTCA 1326
QY 1261 AAGGCGGACTATGTTAGAAAATCTAGACGAAGACAAACAGAGCAAAATTCCTAGAG 1320
Db 1327 AAGGCGGACTATGTTAGAAAATCTAGACGAAGACAAACAGAGCAAAATTCCTAGAG 1386
QY 1321 ATGTTCTCTCTCTTTTGCAGTGGCGCGATGAATTTGAAGATGACGCTGCTCATCTTG 1380
Db 1387 ATGTTCTCTCTCTTTTGCAGTGGCGCGATGAATTTGAAGATGACGCTGCTCATCTTG 1446
QY 1381 AAAATAGAGTTGACATGCTCAACGCTTTTCCAAACGGAAGCACAAGCTGCAATGGAGA 1440
Db 1447 AAAATAGAGTTGACATGCTCAACGCTTTTCCAAACGGAAGCACAAGCTGCAATGGAGA 1506
```

```
QY 1441 TCGCCGAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCGAGCCTGACCGTCTCA 1500
Db 1507 TCGCCGAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCGAGCCTGACCGTCTCA 1566
QY 1501 CTGGTACGAAGAAACATCACCGGTTGAAGATAGCAGCTTTTCAGAAATCCCTAGAAGAGC 1560
Db 1567 CTGGTACGAAGAAACATCACCGGTTGAAGATAGCAGCTTTTCAGAAATCCCTAGAAGAGC 1626
QY 1561 ATCAAACTAGACTAAAGAGCGCTTTCTAAAACCGTGAAGCTCGGGAAACGATTTCTCCCGC 1620
Db 1627 ATCAAACTAGACTAAAGAGCGCTTTCTAAAACCGTGAAGCTCGGGAAACGATTTCTCCCGC 1686
QY 1621 GCTGTTCCGAGTGTCTGACACGATTAATGAATCTGAGAGCTTGAATCAACTGAGCTTGG 1680
Db 1687 GCTGTTCCGAGTGTCTGACACGATTAATGAATCTGAGAGCTTGAATCAACTGAGCTTGG 1746
QY 1681 GAGAAGACGACACTGCTGACAAAACGACTACAAAAGAACGAAAGTACATGGAATACAAG 1740
Db 1747 GAGAAGACGACACTGCTGACAAAACGACTACAAAAGAACGAAAGTACATGGAATACAAG 1806
QY 1741 AGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTCGTCCTGACAG 1800
Db 1807 AGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTCGTCCTGACAG 1866
QY 1801 ATTGACCTTCTCCACATCGAAATCAACCGTGAAGAGGCTTAACCGTAAACTCTCTC 1860
Db 1867 ATTGACCTTCTCCACATCGAAATCAACCGTGAAGAGGCTTAACCGTAAACTCTCTC 1926
QY 1861 ATCGTCGCTGAGACTCTTGGCTCTTAGTGAATTTTGGCTGACCATATATTTCTGT 1920
Db 1927 ATCGTCGCTGAGACTCTTGGCTCTTAGTGAATTTTGGCTGACCATATATTTCTGT 1986
QY 1921 TTTTCATGATGACTGTAATCTGTTTATGCTATCGTGGCGTCATATAGTTTCGCTCTTCGT 1980
Db 1987 TTTTCATGATGACTGTAATCTGTTTATGCTATCGTGGCGTCATATAGTTTCGCTCTTCGT 2046
QY 1981 TTTTCATGCTGTTGTTTATTTGCTGACGCTGCTTCAACAAATTTGTAACAAATTTGAA 2040
Db 2047 TTTTCATGCTGTTGTTTATTTGCTGACGCTGCTTCAACAAATTTGTAACAAATTTGAA 2106
QY 2041 CCAATGTATACAGATTTGTAATATATATTTATGATACATCAACAATA 2087
Db 2107 CCAATGTATACAGATTTGTAATATATATTTATGATACATCAACAATA 2153
```

```
RESULT 3
AR087502 LOCUS AR087502 2011 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from patent US 5986082.
ACCESSION AR087502
VERSION AR087502.1 GI:10014265
KEYWORDS SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2011)
AUTHORS Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.
TITLE Altered forms of the NIM1 gene conferring disease resistance in plants
JOURNAL Patent: US 5986082-A 6 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..2011
BASE COUNT 563 a 417 c 472 g 559 t
ORIGIN
```

```
Query Match 95.5%; Score 2009.4; DB 6; Length 2011;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 51 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACTTGTAT 110
Db 1 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACTTGTAT 60
```


QY 111 GGATTGCGCGATTCTTATGAATCAGACGACTAGTTTCGTCGTACCGATAACACCGAC 170
|||||
Db 61 GGATTGCGCGATTCTTATGAATCAGACGACTAGTTTCGTCGTACCGATAACACCGAC 120
QY 171 TCCTCTATTGTTTATCTGGCCGCGGAACAGTACTCACCAGACCTGATGATCTGCTCTG 230
|||||
Db 121 TCCTCTATTGTTTATCTGGCCGCGGAACAGTACTCACCAGACCTGATGATCTGCTCTG 180
QY 231 CAATTGCTCTCAACAGCTTCGAATCCGTCCTTTGACTCGCGGATGATTTCTACAGCGAC 290
|||||
Db 181 CAATTGCTCTCAACAGCTTCGAATCCGTCCTTTGACTCGCGGATGATTTCTACAGCGAC 240
QY 291 GCTAAGCTTGTCTCTCCGACGCGCGGAAGTTTCTTTCCACCGCTGCGTTTGTCTCAGCG 350
|||||
Db 241 GCTAAGCTTGTCTCTCCGACGCGCGGAAGTTTCTTTCCACCGCTGCGTTTGTCTCAGCG 300
QY 351 AGAAGCTCTTTCTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCAACAAC 410
|||||
Db 301 AGAAGCTCTTTCTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCAACAAC 360
QY 411 ACCGCGCGCTGAAGCTCGAGCTTAAGAGATTTGCCAAGGATTAAGAGTTCGGTTCGAT 470
|||||
Db 361 ACCGCGCGCTGAAGCTCGAGCTTAAGAGATTTGCCAAGGATTAAGAGTTCGGTTCGAT 420
QY 471 TCGGTTGTGACTGTTTGGCTTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGGA 530
|||||
Db 421 TCGGTTGTGACTGTTTGGCTTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGGA 480
QY 531 GTTTCCTGAATCGCAGACGAGAATTGTCACGTCGCTTCCGCGCGCGGCTGGATTTC 590
|||||
Db 481 GTTTCCTGAATCGCAGACGAGAATTGTCACGTCGCTTCCGCGCGCGGCTGGATTTC 540
QY 591 ATGTTGAGGTTTCCTATTGGCTTTTCATCTTCAAGATCCCTGAATTAATCTCTCTAT 650
|||||
Db 541 ATGTTGAGGTTTCCTATTGGCTTTTCATCTTCAAGATCCCTGAATTAATCTCTCTAT 600
QY 651 CAGAGGCACCTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATATCTC 710
|||||
Db 601 CAGAGGCACCTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATATCTC 660
QY 711 AAGCTTGCCTAATATATGTTGTAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT 770
|||||
Db 661 AAGCTTGCCTAATATATGTTGTAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT 720
QY 771 ATTGCTCAAGTCTAATGTAGATATGTTAGTCTTGAAGGTCATTGCCGGAAGAGCTTGT 830
|||||
Db 721 ATTGCTCAAGTCTAATGTAGATATGTTAGTCTTGAAGGTCATTGCCGGAAGAGCTTGT 780
QY 831 AAAGAGATAATTGATAGACCTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT 890
|||||
Db 781 AAAGAGATAATTGATAGACCTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT 840
QY 891 GTCTCGAATGATACATAGGACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950
|||||
Db 841 GTCTCGAATGATACATAGGACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 900
QY 951 AAAGAGGATCACACCAATCTAGATGATGCGTGTGCTTTCATTTCCGCTGTCGATATTGC 1010
|||||
Db 901 AAAGAGGATCACACCAATCTAGATGATGCGTGTGCTTTCATTTCCGCTGTCGATATTGC 960
QY 1011 AATGTGAAGACCGCAACAGATCTTTTAAACHTTGATCTTGGCGATGCTCAACCATAGGAAT 1070
|||||
Db 961 AATGTGAAGACCGCAACAGATCTTTTAAACHTTGATCTTGGCGATGCTCAACCATAGGAAT 1020
QY 1071 CCGAGGGGATATACGGTGTCTCATGTTGCTGCCATCGGAAGAGCCCAATTTGATACFA 1130
|||||
Db 1021 CCGAGGGGATATACGGTGTCTCATGTTGCTGCCATCGGAAGAGCCCAATTTGATACFA 1080
QY 1131 TCCTATTGGAAAAAGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC 1190
|||||
Db 1081 TCCTATTGGAAAAAGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC 1140

QY 1191 ATGATCGCAAAACAAGCCACTATGCGGTTGAATGTAATAATATCCCGGAGCAATGCCAAG 1250
|||||
Db 1141 ATGATCGCAAAACAAGCCACTATGCGGTTGAATGTAATAATATCCCGGAGCAATGCCAAG 1200
QY 1251 CATTTCTCTCAAAGCCGAGCTATGTGTAGAAATACTAGACCAAGAAGCAACAACGAGAACAA 1310
|||||
Db 1201 CATTTCTCTCAAAGCCGAGCTATGTGTAGAAATACTAGACCAAGAAGCAACAACGAGAACAA 1260
QY 1311 ATTCTCTAGAGATGTTCCCTCCCTCTTTTGCAGTGGCGCGCATGAATTTGAAGATGACGCTG 1370
|||||
Db 1261 ATTCTCTAGAGATGTTCCCTCCCTCTTTTGCAGTGGCGCGCATGAATTTGAAGATGACGCTG 1320
QY 1371 CTCGATCTTGAAATAGAGTTGCACCTTGTCTCAACGCTCTTTTCCAACGGAAGCACAAAGCT 1430
|||||
Db 1321 CTCGATCTTGAAATAGAGTTGCACCTTGTCTCAACGCTCTTTTCCAACGGAAGCACAAAGCT 1380
QY 1431 GCAATGAGATCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTGACTAGCCCTCGAGCCT 1490
|||||
Db 1381 GCAATGAGATCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTGACTAGCCCTCGAGCCT 1440
QY 1491 GACCGTCTCAGTGGTACGGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAAATC 1550
|||||
Db 1441 GACCGTCTCAGTGGTACGGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAAATC 1500
QY 1551 CTAGAAGAGCATCAAAGTAGACTAAAGGCGCTTCTTAAACCGTGGAACTCGGGAAACGA 1610
|||||
Db 1501 CTAGAAGAGCATCAAAGTAGACTAAAGGCGCTTCTTAAACCGTGGAACTCGGGAAACGA 1560
QY 1611 TTCTTCCCGCGCTGTTCCGGCAGTGCACAGATTATGAACCTGTGAGGACTTTGACTCAA 1670
|||||
Db 1561 TTCTTCCCGCGCTGTTCCGGCAGTGCACAGATTATGAACCTGTGAGGACTTTGACTCAA 1620
QY 1671 CTGGCTTCGGGAGAGACGACACTGCTGAGAAACGACTACAAAAGAACAAAGGTACATG 1730
|||||
Db 1621 CTGGCTTCGGGAGAGACGACACTGCTGAGAAACGACTACAAAAGAACAAAGGTACATG 1680
QY 1731 GAAATACAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTTGAATTAGGAAATTCG 1790
|||||
Db 1681 GAAATACAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTTGAATTAGGAAATTCG 1740
QY 1791 TCCCTGACAGATTCGACTTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGT 1850
|||||
Db 1741 TCCCTGACAGATTCGACTTTCTTCCACATCGAAATCAACCGGTGGAAAGAGGTCTAACCGT 1800
QY 1851 AAACCTCTCATCTGTCGTCGGTGAGACTCTTCCCTCTTAGTGTAAATTTTGCCTGTACCAT 1910
|||||
Db 1801 AAACCTCTCATCTGTCGTCGGTGAGACTCTTCCCTCTTAGTGTAAATTTTGCCTGTACCAT 1860
QY 1911 ATAATTCCTTTTCATGATGACTGTAACCTGTTTATGCTATGCTGTCGTCATATAGTATT 1970
|||||
Db 1861 ATAATTCCTTTTCATGATGACTGTAACCTGTTTATGCTATGCTGTCGTCATATAGTATT 1920
QY 1971 CGCTCTTCGTTTTCATCCTCTGTTATTATGCTGCAGGTGTGCTTCAACAAATGTTGTA 2030
|||||
Db 1921 CGCTCTTCGTTTTCATCCTCTGTTATTATGCTGCAGGTGTGCTTCAACAAATGTTGTA 1980
QY 2031 ACAATTTGAAACCAATGGTATACAGATTGTA 2061
|||||
Db 1981 ACAATTTGAAACCAATGGTATACAGATTGTA 2011

RESULT 4
AF087503
LOCUS AR087503
DEFINITION Sequence 7 from patent US 5986082.
ACCESSION AR087503
VERSION AR087503.1
KEYWORDS GI:10014266
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2011)
AUTHORS Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.

TITLE	Altered forms of the NIM1 gene conferring disease resistance in plants
JOURNAL	US 5986082-A 7 16-NOV-1999;
FEATURES	Location/Qualifiers 1..2011
SOURCE	/organism="unknown"
BASE COUNT	563 a 417 c 474 g 557 t
ORIGIN	
Query Match	95.4%; Score 2006.2; DB 6; Length 2011;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 2008:	Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	51 GATCTCTTAATTGTGTAATTTCAATTCATCGGAACCTGGTTCATGGACACCATTCAT 110
Db	1 GATCTCTTAATTTGTGAAATTTCAATTCATCGGAACCTGGTTCATGGACACCATTCAT 60
Qy	111 GGATTCGCCGAGTTCTTATGAATCAGCAGCACTAGTTTTCTGCCTACCAGATAAACCCGAC 170
Db	61 GGATTCGCCGAGTTCTTATGAATCAGCAGCACTAGTTTTCTGCCTACCAGATAAACCCGAC 120
Qy	171 TCCCTCATTTGTTTATCTGGCGCGCAACAAGTACTCACCGACCTGATGTATCTGCTCTG 230
Db	121 TCCTCTATTTGTTTATCTGGCGCGCAACAAGTACTCACCGACCTGATGTATCTGCTCTG 180
Qy	231 CAATTTGCTCTCCAACAGCTTCGAATCCGCTTTTGACTCGCGGATGATTTCTACAGCGAC 290
Db	181 CAATTTGCTCTCCAACAGCTTCGAACCCGCTTTGACGCGCGGATGATTTCTACAGCGAC 240
Qy	291 GCTAAGCTTGTTCCTCCGACGGCGGGAAGTTCTTTTCCACCGTGCCTTTTGTACGG 350
Db	241 GCTAAGCTTGTTCCTCCGACGGCGGGAAGTTCTTTTCCACCGTGCCTTTTGTACGG 300
Qy	351 AGAAGCTCTTTCTCAAGANGCCTTTAGCCCGCTTAAGAAGGAAAGACTCCAACAC 410
Db	301 AGAAGCTCTTTCTCAAGANGCCTTTAGCCCGCTTAAGAAGGAAAGACTCCAACAC 360
Qy	411 ACCGCGCGCGTAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 470
Db	361 ACCGCGCGCGTAGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 420
Qy	471 TCGGTTGTCACTGTTTGGCTTATGTTTACAGCAGCAGATGAGACCGCGCTTAAGGA 530
Db	421 TCGGTTGTCACTGTTTGGCTTATGTTTACAGCAGCAGATGAGACCGCGCTTAAGGA 480
Qy	531 GTTTCCTGAATGCGCAGACGAAATTCCTGCCACGTGGCTTGGCGCGCGCGTGGATTC 590
Db	481 GTTTCCTGAATGCGCAGACGAAATTCCTGCCACGTGGCTTGGCGCGCGCGTGGATTC 540
Qy	591 ATGTTGGAGTTCTCTATTGGCTTTCATCTTCAGATCCCCTGAATTAATTACTCTAT 650
Db	541 ATGTTGGAGTTCTCTATTGGCTTTCATCTTCAGATCCCCTGAATTAATTACTCTAT 600
Qy	651 CAGAGGCACCTTATTGGACGTTCTAGCAAAGTTGTTATAGAGACACATTCGTTTACTTC 710
Db	601 CAGAGGCACCTTATTGGACGTTCTAGCAAAGTTGTTATAGAGACACATTCGTTTACTTC 660
Qy	711 AAGCTTGTCTAATATATGTGGTAAAGCTTGATGAAGCTATTGGATAGATGTAAGAGATT 770
Db	661 AAGCTTGTCTAATATATGTGGTAAAGCTTGATGAAGCTATTGGATAGATGTAAGAGATT 720
Qy	771 ATTGTCAAGTCTAATGTAGATATGTTAGTCTGAAAAGCTATTGCCGGAAGAGCTTGT 830
Db	721 ATTGTCAAGTCTAATGTAGATATGTTAGTCTGAAAAGCTATTGCCGGAAGAGCTTGT 780
Qy	831 AAAGAGATAAATGTATAGACGTTAAAGAGCTTGCTTTGGAGCTACCTAAAGTAAAGAAACAT 890
Db	781 AAAGAGATAAATGTATAGACGTTAAAGAGCTTGCTTTGGAGGTACCTAAAGTAAAGAAACAT 840
Qy	891 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950
Db	841 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 900


```
/gene="F15H21.11"
/codon_start=1
/product="UDP-galactose 4-epimerase, putative; 6572-4109"
/protein_id="AAG51709.1"
/db_xref="GI:12323470"
/translat="MVGNILVFGAGYIGSHVTQLQLLGGYNTVVVIDLNRSLVSIQ
RYKDLAQHQLMTVHQDLRKPALKRVFSETKFDVAMHVFAGLKAVGESVAKPLLY
NNLLATITLLEMAHGCCKLVFSSATVVGWPKVEPTBESPLSGMSPYGRKLFY
EDICRDVQGRDPEWRIIMLYENPVYGAHPSGRIGEDPGCTPNLMLPYVQVVGRLPN
LKIYGDYITDKGTGVRDIITHVDDIADHGICALQKLDDETEIGCEVYNLKGKTYLE
MYDAFEKASGMKIPLVKVRGRRPGDAETVYASTEKAERUNLNKAFIEEMCRDQWNWA
SNPFYGSPPNST"
complement(join(6810..6979,7311..7400,7552..7605,
7688..7759,7853..7940,8028..8095,8180..8287,8409..8792,
9058..9106,9145..9224,9310..9387,9478..9629,9686..10294))
/gene="F15H21.10"
complement(6810..10294)
/gene="F15H21.10"
complement(join(7338..7400,7552..7605,7688..7759,
7853..7940,8028..8095,8180..8287,8409..8792,9058..9106,
9145..9224,9310..9387,9478..9629,9686..10133))
/gene="F15H21.10"
/codon_start=1
/product="unknown protein; 10133-7338"
/protein_id="AAG51706.1"
/db_xref="GI:12323467"
/translat="MSLRVSVSSFGINRPNLHETHTLRSHVFSFFPKPANIGSIR
RLVSPYGRDRSDVGSADVSSYLLDDELLSSVAVRDADEALAMISDRPGSNRGG
IVLEDCRSIIIAAIVSRGNVDLALISFYITMRASFOLDGLTILSTLLTQSGDNDRWSW
RPDEVYITMLNGLAASRLVSDLSRIIRICRVGSPAEVFPFKIVICPSCSLIAIV
AOPHQVQIVCANRQYQYELFSIDSEELSGRKVIQIMLGAVRAVFPVTPSGT
ATHREATFELPAQEGRVITIASAAPSNVYRVGPVKFISKAPNFYGPPEMSLTGH
KDGRESILLRPSKQDKILOPSEFLIPLAILATGDAAGVDPDLSPLLVSATVTSL
AGATLPERTVVGILLQOLLSSQYDVLQRRIDRLKEAVEKEVWMLARCOLENNILAV
GEPAYTRTRVKKVRESLENSIKYDILRISYARISSWIEIEVEVMSDVLAEAVNN
TENIAQIEQIMLENELEEKWKIQAPANDEAPRLSSQP"
complement(10465..10537)
/gene="60083.trna-Ala-1"
/product="trna-Ala"
complement(10465..10537)
/gene="60083.trna-Ala-1"
join(<11471..11617,11714..11766,12058..12191,12213..12309,
12686..12786,13367..13702,13835..13925,14904..15298,
15418..>16325)
/gene="F15H21.18"
11471..16325
/gene="F15H21.18"
join(11471..11617,11714..11766,12058..12191,12213..12309,
12686..12786,13367..13702,13835..13925,14904..15298,
15418..16325)
/gene="F15H21.18"
/codon_start=1
/product="unknown protein; 11471-16325"
/protein_id="AAG51717.1"
/db_xref="GI:12323478"
/translat="MDEVSPYTAIKNLKPKFTSWCTQVKILHAWNHYTKSGMSYEMM
LADGNKIOAGKKKELHLQSLDELAKHFENIRAYNMLFSFTISGKVDHCLPKG
RPNMFAIOGALPKPSVAKAKFOOLYIVDTENEVNNRYIMRLRYIKNNOPFRSNK
ESTONASNSGNLENGMYTIEFOKRGPLPHAILLFMHPTSKLSTABTDKVIITAEI
PDKKAFELFVYVKDCMIHGPGVGHPSFCMHENGKCKKFFPKSYSDITTKVDNDGFPV
Query Match 83.7%; Score 1761; DB 8; Length 96887;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 297; Gaps 3;
Qy 1 TCGATCTTTACCAAAATCCAGTTGATAGGTCCTTCGTTGATTAGCAGAGATCTCTTA 60
Db 88175 TCGATCTTTTAAACCAATCCAGTTGATAGGTCCTTCGTTGATTAGCAGAGATCTCTTTA 88234
Qy 61 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCAATTCATGATTCGCCG 120
Db 88235 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCAATTCATGATTCGCCG 88294
```


Db	4375	CGTCTCACCTGGTTACGAAGAAGACATACACGGGTGTAAGAATAGCACCTTTTCAGAATCCTA	4435
Qy	1554	GAAGAGCATCAAAAGTAGACTAAAGCGCTTTCTTCAAAACC-----	1592
Db	4435	GAAGAGCATCAAAAGTAGACTAAAGCGCTTTCTTCAAAACCGGTATGGA'TTCTCAOCCACTT	4494
Qy	1593	-----	1592
Db	4495	CATCGGACTCCTTTATCACAAAAACAAACTAAATGATCTTTTAAACATGGT'TTGTGTACT	4554
Qy	1593	-----GTGGAACTCGGGAAACAGATTTCTCCCGCGC	1622
Db	4555	TGCTGCTGCACCTTGTTTTTTTATCATCAGTGGAACTCGGGAACAGATTTCTTCCCGCGC	4614
Qy	1623	TGTTGGCAGTGCCTGACACAGATTAATGAACCTGTGAGGACTTGACTCAACTGCCTTGC	1682
Db	4615	TGTTGGCAGTGCCTGACACAGATTAATGAACCTGTGAGGACTTGACTCAACTGCCTTGC	4674
Qy	1683	GAAGACGACACTGCTCGAAGACACTACAAAAGAACGAAAGCTACATGGAATACAAAG	1742
Db	4675	GAAGACGACACTGCTCGAAGACACTACAAAAGAACGAAAGCTACATGGAATACAAAG	4734
Qy	1743	ACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAAATTAGGAAATTCGTCCTGACAGAT	1802
Db	4735	ACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAAATTAGGAAATTCGTCCTGACAGAT	4794
Qy	1803	TCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGCTCTAACGGTAAACTCTCTCAT	1862
Db	4795	TCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGCTCTAACGGTAAACTCTCTCAT	4854
Qy	1863	CGTCGTCGGTGAGACTCTTGCCCTCTTAGTGTAATTTTTCGCTGACCATATAATCTGTTT	1922
Db	4855	CGTCGTCGGTGAGACTCTTGCCCTCTTAGTGTAATTTTTCGCTGACCATATAATCTGTTT	4914
Qy	1923	TCATGATGACGTAACTGGTTTTATGCTATCGTTGGCGCTCATATAGTTTCGCTTCGTTT	1982
Db	4915	TCATGATGACGTAACTGGTTTTATGCTATCGTTGGCGCTCATATAGTTTCGCTTCGTTT	4974
Qy	1983	TGCATCTGTTGTAATTATGCTGCAGGTGTCCTTCAACAAATTTGTTGAACAATTTGAACC	204
Db	4975	TGCATCTGTTGTAATTATGCTGCAGGTGTCCTTCAACAAATTTGTTGAACAATTTGAACC	503
Qy	2043	AATGGTATACAGATTTGTAATATATATTATGATACATCAACAATAA	2088
Db	5035	AATGGTATACAGATTTGTAATATATATTATGATACATCAACAATAA	5080
RESULT 7			
ATU87794			
LOCUS	ATU87794	5655 bp	DNA linear
DEFINITION	Arabidopsis thaliana transcription factor inhibitor I kappa B homolog (nim1) gene, complete cds.		
ACCESSION	U87794		
VERSION	U87794.1	GI:1916911	
KEYWORDS			
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Ryals,J., Weymann,K., Lawton,K., Friedlich,L., Ellis,D., Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and Uknes,S.		
TITLE	The Arabidopsis NIM1 protein shows homology to the mammalian transcription factor inhibitor I kappa B		
JOURNAL	Plant Cell 9 (3), 425-439 (1997)		
MEDLINE	97246324		
REFERENCE	2 (bases 1 to 5655)		
AUTHORS	Ryals,J., Weymann,K., Lawton,K., Friedlich,L., Ellis,D., Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and Uknes,S.		
TITLE	Direct Submission		

JOURNAL Submitted (29-JAN-1997) Fungicides, Novartis BGC, 3054 Cornwallis
Road, Research Triangle Park, NC 27709, USA
FEATURES Location/Qualifiers
source 1..5655
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
/map="between ATHGENEA and ngall1"
join(2754..3347,3427..4162,4271..4474,4586..5053)
2787..4866
/gene="nml"
join(2787..3347,3427..4162,4271..4474,4586..4866)
/gene="nml"
/codon_start=1
/product="transcription factor inhibitor I kappa B
homolog"
/protein_id="AAB58262.1"
/db_xref="GI:1916912"
/translation="MDTIDGFADSYEISSTSFVATDNTDSSIVLYAAEQVLTPDVS
ALQLNSFSEVSDPDYDAKLVLSDGREVSFHRCLVSARSFFKSALAAKKEK
DSNNTAAVKLELKEIAKDYEVGDSVTVLAVYSSRVPPPKYSECADENCCHVAC
RPVDFMLEVLYLAFIPKIPELITLQRLHLDVYKVVIEDTLVLKLANICGKACMK
LDRCKEIIIVKSNVDMVSEKSLPEELVKEIDRRKELGLEVPKVKHVSNNYKALDS
DDIELVLLKDEHTNLDACALHFAVCNVTATDCLKLIDLADNVNHNPKGYTLVH
VAANKPEQLISLLEKASASEATLEGRTALMIAKOATMAVECNINPEQKHSIKGR
LCVILSQEDKRSGIIPKDVPPSPFAVADELKMTLLDLENRVLAORLPFTEAQAAMEI
AEMKGTCFEIVTSLEPRLTGRTSPGVKIAPFRILEHQSLKALSRTVBLGRFF
PRSAVLDTQNCEDITQLACEDDTAEKRLQKRYMBIOETLKAFFSEDNLELGS
SLDTSSTSTSKSTGGKRSNKLSHRRR"
BASE COUNT 1758 a 1014 c 1069 g 1814 t
ORIGIN
Query Match 83.7%; Score 1760; DB 8; Length 5655;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;
QY 1 TCGATCTTTAAACCAATCCAGTGTGATAGGTCCTTCGTTGATPAGCAGAGATCTCTTTA 60
DB 2695 TCGATCTTTAAACCAATCCAGTGTGATAGGTCCTTCGTTGATPAGCAGAGATCTCTTTA 2754
QY 61 ATTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACACATTCATGATGCGCG 120
DB 2755 ATTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACACATTCATGATGCGCG 2814
QY 121 ATTCTTATGAATCAGCAGACTAGTTTCGTCGCTACCGATACACGACTCCCTCTATTG 180
DB 2815 ATTCTTATGAATCAGCAGACTAGTTTCGTCGCTACCGATACACGACTCCCTCTATTG 2874
QY 181 TTATCTGCGCGCGGAACTACTACCGGACCTGATGTATCTGCTCTGCAATTTGCTCT 240
DB 2875 TTATCTGCGCGCGGAACTACTACCGGACCTGATGTATCTGCTCTGCAATTTGCTCT 2934
QY 241 CCAACAGCTTGAATTCGCTCTTGACTCGCGGATGATTTCTACGACGAGCTTAAGCTTG 300
DB 2935 CCAACAGCTTGAATTCGCTCTTGACTCGCGGATGATTTCTACGACGAGCTTAAGCTTG 2994
QY 301 TTCTCTCCGACGCGCGGAAAGTTTCTTTCCACCGGTGCGTTTGTCTACGCGAGAAGCTT 360
DB 2995 TTCTCTCCGACGCGCGGAAAGTTTCTTTCCACCGGTGCGTTTGTCTACGCGAGAAGCTT 3054
QY 361 TCTTCAAGAGCGCTTTAGCGCGCGGTAGAGAGAGAAAGACTCCAAACACCGCGCGCG 420
DB 3055 TCTTCAAGAGCGCTTTAGCGCGCGGTAGAGAGAGAAAGACTCCAAACACCGCGCGCG 3114
QY 421 TGAAGCTCGAGCTTAAGGAGATTGCAAGGATTACGAAGTCGGTTTCGATTTCGGTTCTGA 480
DB 3115 TGAAGCTCGAGCTTAAGGAGATTGCAAGGATTACGAAGTCGGTTTCGATTTCGGTTCTGA 3174
QY 481 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAGAGGAGTTTCTGAAT 540
DB 3175 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAGAGGAGTTTCTGAAT 3234

QY 541 GCGCAGACGAGAATTGCTGCCACGTGGCTTCCGCGCGCGGCTGGATTTCATCTGTTGAGG 600
DB 3235 GCGCAGACGAGAATTGCTGCCACGTGGCTTCCGCGCGCGGCTGGATTTCATCTGTTGAGG 3294
QY 601 TTCCTATTTGGCTTTCACTTCAAGATCCCTGAATTAATTAATCTCTA----- 649
DB 3295 TTCCTATTTGGCTTTCACTTCAAGATCCCTGAATTAATTAATCTCTATCAGGTAAC 3354
QY 650 ----- 649
DB 3355 ACCATCTGCATTAAGCTATGCTTACACATTCATCAATATGTTCTTACTTGGTACTTGA 3414
QY 650 -----TCAGAGCAGCTTATTGGAGCGTTGTAGACAAAAGTTGTTATAGAGACACATTG 701
DB 3415 TTGTGATTTCAGAGCAGCTTATTGGAGCGTTGTAGACAAAAGTTGTTATAGAGACACATTG 3474
QY 702 GTTATACTCAAGCTTGTCTAATATATGTTGTAAGCTTGTATGAAGCTATTGGATAGATGT 761
DB 3475 GTTATACTCAAGCTTGTCTAATATATGTTGTAAGCTTGTATGAAGCTATTGGATAGATGT 3534
QY 762 AAAGAGATTATGCAAGCTAATGTTAGATGATGTTAGTCTTGAAGAGTCAATTCGCCGAA 821
DB 3535 AAAGAGATTATGCAAGCTAATGTTAGATGATGTTAGTCTTGAAGAGTCAATTCGCCGAA 3594
QY 822 GAGCTTGTAAAGAGATAAATGATAGAGTAAGAGCTTGGTTGGAGGTAACCTAAAGTA 881
DB 3595 GAGCTTGTAAAGAGATAAATGATAGAGTAAGAGCTTGGTTGGAGGTAACCTAAAGTA 3654
QY 882 AAGAACAATGCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGATGATCAAG 941
DB 3655 AAGAACAATGCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGATGATCAAG 3714
QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGGTGTGCTCTTCATTTCCGCTGTT 1001
DB 3715 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGGTGTGCTCTTCATTTCCGCTGTT 3774
QY 1002 GCATATGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTGCGGATGTCAAC 1061
DB 3775 GCATATGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTGCGGATGTCAAC 3834
QY 1062 CATAGAAATCCGAGGGGATATACGGTGTTCATGTTGCTGCGATGCGGAGAGGCCACAA 1121
DB 3835 CATAGAAATCCGAGGGGATATACGGTGTTCATGTTGCTGCGATGCGGAGAGGCCACAA 3894
QY 1122 TTGATCTATCTCTAATGGAAGAGGTCAGTGCATCAGAACCACTTTTGAAGGTAGA 1181
DB 3895 TTGATCTATCTCTAATGGAAGAGGTCAGTGCATCAGAACCACTTTTGAAGGTAGA 3954
QY 1182 ACCGCACTCATGATCGCAAAACAAAGCCACTATGGCGGTTGAATGTAATATATATCCCGGAG 1241
DB 3955 ACCGCACTCATGATCGCAAAACAAAGCCACTATGGCGGTTGAATGTAATATATATCCCGGAG 4014
QY 1242 CAATCAAGCAATCTCTCAAGAGCGGACTATGTAGAAATACTAGAGCAAGAGACAAA 1301
DB 4015 CAATCAAGCAATCTCTCAAGAGCGGACTATGTAGAAATACTAGAGCAAGAGACAAA 4074
QY 1302 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGGATGAAATGAAG 1361
DB 4075 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGGATGAAATGAAG 4134
QY 1362 ATGACGCTGCTGATCTTTGAAATAG----- 1387
DB 4135 ATGACGCTGCTGATCTTTGAAATAGAGGTATCTATCAAGTCTTATTCTTATATGTTTG 4194
QY 1388 ----- 1387
DB 4195 AATTAATTTATGCTCTCTCTATTAGGAACTGAGTGAACCTAATGATAACTATTCTTTGT 4254
QY 1388 -----ASTTGCACCTGCTCAAGCTCTTTTCCACGGAAGCAAGCTGCA 1433
DB 4255 GTCTCCACCTGTTTATGTTGCTCAAGCTCTTTTCCACGGAAGCAAGCTGCA 4314
QY 1434 ATGGAGTCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCTCGACCTGAC 1493

Db	4315	ATGGAGATCCCGAAATGAAGGAAACATGTGAGTTTCATAGTGTGCTAGCCTCGAGCCTGAC	4374	
Qy	1494	CGTCTCACTGGTACGAAGAGAACATCACCGGGTGAAGATAGCACCCTTTCAGAAATCCTA	1553	
Db	4375	CGTCTCACTGGTACGAAGAGAACATCACCGGGTGAAGATAGCACCCTTTCAGAAATCCTA	4434	
Qy	1554	GAAGAGCATCAAGTAGACTAAAGCGCTTCTTAAACC-----	1592	
Db	4435	GAAGAGCATCAAGTAGACTAAAGCGCTTCTTAAACC-----	4494	
Qy	1593	-----	1592	
Db	4495	CATCGGACTCCTTATCACAAAAACAAACTAAATGATCTTTAAACATGGTTTGTACT	4554	
Qy	1593	-----GTGGAACCTCGGGAACGATCTTCCCGCGC	1622	
Db	4555	TGCTGTCTGACCTTGTTTTTTTATCATCATGTAAGTCTCGGGAACGATCTTCCCGCGC	4614	
Qy	1623	TGTTCCGAGTGTGCGACCATATATCAACTGTGAGACTTGACTCAACTGGCTTCGGGA	1682	
Db	4615	TGTTCCGAGTGTGCGACCATATATCAACTGTGAGACTTGACTCAACTGGCTTCGGGA	4674	
Qy	1683	GAAGCAGACACTGCTGAGAACGACTACAAAAGAACAAAGGTACATGGAATACAAGAG	1742	
Db	4675	GAAGCAGACACTGCTGAGAACGACTACAAAAGAACAAAGGTACATGGAATACAAGAG	4734	
Qy	1743	ACACTAAAGAGGCTTTAGTAGGACAAATTTGGAATTAGGAATTCGTCCTCGACAGAT	1802	
Db	4735	ACACTAAAGAGGCTTTAGTAGGACAAATTTGGAATTAGGAATTCGTCCTCGACAGAT	4794	
Qy	1803	TCGACTTCTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT	1862	
Db	4795	TCGACTTCTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT	4854	
Qy	1863	CGTGGTGGTGGAGACTCTGTGCTCTTATGCTATCGTTGGCGTCAATATAGTTCTCGTTT	1922	
Db	4855	CGTGGTGGTGGAGACTCTGTGCTCTTATGCTATCGTTGGCGTCAATATAGTTCTCGTTT	4914	
Qy	1923	TCATGATGACTGTAACTGCTTTATGCTATCGTTGGCGTCAATATAGTTCTCGTTT	1982	
Db	4915	TCATGATGACTGTAACTGCTTTATGCTATCGTTGGCGTCAATATAGTTCTCGTTT	4974	
Qy	1983	TGCACTCTGTGTATPATTCGTCGAGGTGCTTCAACAAATGTGTAACTTTGAACC	2042	
Db	4975	TGCACTCTGTGTATPATTCGTCGAGGTGCTTCAACAAATGTGTAACTTTGAACC	5034	
Qy	2043	AATGATATACAGATTTGTAATATATATTTATGATACATCAACAATAA	2088	
Db	5035	AATGATATACAGATTTGTAATATATATTTATGATACATCAACAATAA	5080	
RESULT 8				
AR087505				
LOCUS				
DEFINITION				
AR087505				
ACCESSION				
AR087505.1				
KEYWORDS				
SOURCE				
ORGANISM				
Unclassified.				
1 (bases 1 to 1608)				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
BASE COUNT				
ORIGIN				

Query Match				
Best Local Similarity 76.3%; Score 1605; DB 6; Length 1608;				
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	51	GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCACCATTTGAT	110	
Db	1	GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCACCATTTGAT	60	
Qy	111	GGATTCCGCGGATTCCTTATGAAATCAGCAGCAGCTAGTTTCGTCGCTACCGATAACACCGAC	170	
Db	61	GGATTCCGCGGATTCCTTATGAAATCAGCAGCAGCTAGTTTCGTCGCTACCGATAACACCGAC	120	
Qy	171	TCCTCTATTTGTTTATCTGCGCGCGGAAACAGTACACCGGACCTGATGATCTGCTCTG	230	
Db	121	TCCTCTATTTGTTTATCTGCGCGCGGAAACAGTACACCGGACCTGATGATCTGCTCTG	180	
Qy	231	CAATTGCTCTCAACAGCTTCGAATCCGCTCTTGGACTCGCGGATGATTTCTACAGCGAC	290	
Db	181	CAATTGCTCTCAACAGCTTCGAATCCGCTCTTGGACTCGCGGATGATTTCTACAGCGAC	240	
Qy	291	GCTAAGCTTGTCTCTCCGACGCGCGGGAAGTTCTTCCACCGGTGCGTTTGTACGCG	350	
Db	241	GCTAAGCTTGTCTCTCCGACGCGCGGGAAGTTCTTCCACCGGTGCGTTTGTACGCG	300	
Qy	351	AGAAGCTCTTCTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCCAACAC	410	
Db	301	AGAAGCTCTTCTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCCAACAC	360	
Qy	411	ACCGCGCGCTGAAGCTCGAGCTTAAGGAGATTCGCAAGGATTACGAAGTCGGTTTCGAT	470	
Db	361	ACCGCGCGCTGAAGCTCGAGCTTAAGGAGATTCGCAAGGATTACGAAGTCGGTTTCGAT	420	
Qy	471	TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTACAGCCGCGCTTAAGGA	530	
Db	421	TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTACAGCCGCGCTTAAGGA	480	
Qy	531	GTTTCTGAATGSCACACGAGAAATGCTGCCACGTGGCTTGGCGCGCGGTGGATTTC	590	
Db	481	GTTTCTGAATGSCACACGAGAAATGCTGCCACGTGGCTTGGCGCGCGGTGGATTTC	540	
Qy	591	ATGTTGGAGGTCTCTATTTGGCTTCATCTCAAGATCCCTGAATTAATTACTCTCTAT	650	
Db	541	ATGTTGGAGGTCTCTATTTGGCTTCATCTCAAGATCCCTGAATTAATTACTCTCTAT	600	
Qy	651	CAGAGCAGCTTATGACGCTTGTAGACAAAGTTGTTATAGAGACACATTTGGTTATACTC	710	
Db	601	CAGAGCAGCTTATGACGCTTGTAGACAAAGTTGTTATAGAGACACATTTGGTTATACTC	660	
Qy	711	AAGCTTGCCTAATATATGTTGAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT	770	
Db	661	AAGCTTGCCTAATATATGTTGAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT	720	
Qy	771	ATTGTCGAAGTCTAATGTAGATATGTTAGTCTTGAAGATCATTCGCGAAGAGCTTGT	830	
Db	721	ATTGTCGAAGTCTAATGTAGATATGTTAGTCTTGAAGATCATTCGCGAAGAGCTTGT	780	
Qy	831	AAAGAGATAATTTGATAGACCTTAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACAT	890	
Db	781	AAAGAGATAATTTGATAGACCTTAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACAT	840	
Qy	891	GTCTCGAATGTACATAAGGACCTTGACTCGGATGATATTGAGTTAGTTCAGTTGCTTTTG	950	
Db	841	GTCTCGAATGTACATAAGGACCTTGACTCGGATGATATTGAGTTAGTTCAGTTGCTTTTG	900	
Qy	951	AAAGAGGATCACACCAATCTAGATGATGCGTCTCTTCATTTCCGCTGTTGCATATTGC	1010	
Db	901	AAAGAGGATCACACCAATCTAGATGATGCGTCTCTTCATTTCCGCTGTTGCATATTGC	960	
Qy	1011	AATGTGAAGCCGCAACAGATCTTTTAAACTTGTATCTTCCCGATGTCAACACCATAGGAAT	1070	
Db	961	AATGTGAAGCCGCAACAGATCTTTTAAACTTGTATCTTCCCGATGTCAACACCATAGGAAT	1020	
Qy	1071	CCGAGGGGATATACGGTCTTCATGTTGCTGCGATCGGAAGGAGCCAACTTGTACTA	1130	

```
|||||
Db 1021 CCGAGGGATATACGGTGCCTTCATGTCGATGCGGAAGGAGCCACAAATTGATACTA 1080
QY 1131 TCCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAGGTAGAACCGCACTC 1190
Db 1081 TCCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAGGTAGAACCGCACTC 1140
QY 1191 ATGATCGCAAAACAAGCCACTATGGCGTTGAATGTAATAATATCCCGGAGCAATGCAAG 1250
Db 1141 ATGATCGCAAAACAAGCCACTATGGCGTTGAATGTAATAATATCCCGGAGCAATGCAAG 1200
QY 1251 CATTCCTCAAAAGCCGACTATGTGTAGAAATACTAGAGCAAGAGACAAACGAGAACAA 1310
Db 1201 CATTCCTCAAAAGCCGACTATGTGTAGAAATACTAGAGCAAGAGACAAACGAGAACAA 1260
QY 1311 ATTCCTAGAGATGTTCCCTCCCTCTTTTCAGTGGCGCGGATGAATTCAGATCAGCGTG 1370
Db 1261 ATTCCTAGAGATGTTCCCTCCCTCTTTTCAGTGGCGCGGATGAATTCAGATCAGCGTG 1320
QY 1371 CTCGATCTTGAATATAGAGTTGCACCTTCTCAAGCTCTTTTCCAAACGGAAGCACAAGCT 1430
Db 1321 CTCGATCTTGAATATAGAGTTGCACCTTCTCAAGCTCTTTTCCAAACGGAAGCACAAGCT 1380
QY 1431 GCAATGGAGATCGCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCGAGCCT 1490
Db 1381 GCAATGGAGATCGCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCGAGCCT 1440
QY 1491 GACCGTCTCAGTGGTACGAAGAGACATCACC GGGTGTAAGATAGACCTTTTCAGATC 1550
Db 1441 GACCGTCTCAGTGGTACGAAGAGACATCACC GGGTGTAAGATAGACCTTTTCAGATC 1500
QY 1551 CTAGAAGAGCATCAAGTAGACTAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGA 1610
Db 1501 CTAGAAGAGCATCAAGTAGACTAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGA 1560
QY 1611 TTCCTCCGCGCTGTTCCGCGAGTGTCTGACCGAGTGTCTGACAGATTAATGAAGTGT 1655
Db 1561 TTCCTCCGCGCTGTTCCGCGAGTGTCTGACCGAGTGTCTGACAGATTAATGAAGTGT 1605

RESULT 9
AR087504
LOCUS AR087504 1597 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 9 from patent US 5986082.
ACCESSION AR087504
VERSION AR087504.1 GI:10014267
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1597)
AUTHORS Uknes, S. Joseph, Hunt, M. Denise, Steiner, H. and Ryals, J. Andrew.
TITLE Altered forms of the NIM1 gene conferring disease resistance in plants
JOURNAL Patent: US 5986082-A 9 16-NOV-1999;
FEATURES
    Location/Qualifiers
        source
            1. .1597
                /organism="unknown"
BASE COUNT 467 a 304 c 381 g 445 t
ORIGIN
Query Match 75.7%; Score 1592.8; DB 6; Length 1597;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 TCGATTCCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTA 525
Db 2 TGGATTCCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTA 61
QY 526 RAGGATTTCTCAATGCCACACAGATTTCTGCCAGTGGCTTCCGGCGCGCGGTGG 585
Db 62 AAGGATTTCTCAATGCCACACAGATTTCTGCCAGTGGCTTCCGGCGCGCGGTGG 121
```

```
QY 586 ATTTCATGTTGGAGTTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTACTC 645
Db 122 ATTCATGTTGGAGTTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTACTC 181
QY 646 TCATCAGAGGCACTTATTTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTA 705
Db 182 TCATCAGAGGCACTTATTTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTA 241
QY 706 TACTCAAGCTTGCTAATATATGTTGTAAGCTTGATGAAGCTATTGGATAGATGTAAG 765
Db 242 TACTCAAGCTTGCTAATATATGTTGTAAGCTTGATGAAGCTATTGGATAGATGTAAG 301
QY 766 AGATTATTGTCAAAGTCTAATGTAGATATGTTAGTCTTGAAGAGTCAATGCCGGAAGAGC 825
Db 302 AGATTATTGTCAAAGTCTAATGTAGATATGTTAGTCTTGAAGAGTCAATGCCGGAAGAGC 361
QY 826 TTGTTAAAGAGATAAATGTATAGACGTAAGAGCTTGGTTTGGAGGTACCTTAAAGTAAAGA 885
Db 362 TTGTTAAAGAGATAAATGTATAGACGTAAGAGCTTGGTTTGGAGGTACCTTAAAGTAAAGA 421
QY 886 AACATGCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGC 945
Db 422 AACATGCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGC 481
QY 946 TTTTGAAGAGGATCACACCAATCTAGATGCGTGTGCTCTTCATTTTCGCTGTTGTCAT 1005
Db 482 TTTTGAAGAGGATCACACCAATCTAGATGCGTGTGCTCTTCATTTTCGCTGTTGTCAT 541
QY 1006 ATTGCAATGTGAAGACGCGCAACAGATCTTTTAAAACTTGATTTGCCGATGTCAACCAT 1065
Db 542 ATTGCAATGTGAAGACGCGCAACAGATCTTTTAAAACTTGATTTGCCGATGTCAACCAT 601
QY 1066 GGAATCGAGGGGATATACGGTCTTCATGTTGCTCGGATCGGGAAGGAGCCACAATTGA 1125
Db 602 GGAATCGAGGGGATATACGGTCTTCATGTTGCTCGGATCGGGAAGGAGCCACAATTGA 661
QY 1126 TACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGGAGGTAGAACCG 1185
Db 662 TACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGGAGGTAGAACCG 721
QY 1186 CACTCATGATCGCAAAACAAGCCACTATGCGGTTTGAATGTAATAATATCCCGGAGCAAT 1245
Db 722 CACTCATGATCGCAAAACAAGCCACTATGCGGTTTGAATGTAATAATATCCCGGAGCAAT 781
QY 1246 GCAAGCATTTCTCTCAAGGCGGACTATGTGTAAATACTAGAGCAAGAGACAAACGAG 1305
Db 782 GCAAGCATTTCTCTCAAGGCGGACTATGTGTAAATACTAGAGCAAGAGACAAACGAG 841
QY 1306 AACAAATTCCTAGAGATGTTCCCTCCCTCTTTTCAGTGGCGCGGATGAATTCGAAGATGA 1365
Db 842 AACAAATTCCTAGAGATGTTCCCTCCCTCTTTTCAGTGGCGCGGATGAATTCGAAGATGA 901
QY 1366 CGTGCTCGATCTTGAAAAATAGAGTTGCACTTCTCTCAACGTCCTTTTCCAAACGGAAGCAC 1425
Db 902 CGTGCTCGATCTTGAAAAATAGAGTTGCACTTCTCTCAACGTCCTTTTCCAAACGGAAGCAC 961
QY 1426 AAGCTCAATGGAGATCGCGCAATGAGGGAACATGTGAGTTTCATAGTACTAGCCTCG 1485
Db 962 AAGCTCAATGGAGATCGCGCAATGAGGGAACATGTGAGTTTCATAGTACTAGCCTCG 1021
QY 1486 AGCTGACCCGCTCTCACTGTGTACGAAGAACATCACC GGGTGTAAAGATAGCACCTTTCA 1545
Db 1022 AGCTGACCCGCTCTCACTGTGTACGAAGAACATCACC GGGTGTAAAGATAGCACCTTTCA 1081
QY 1546 GAATTCCTAGAAAGAGCATCAAAGTAGACTAAAGCGCTTCTTAAACCGTGGAACTCGGGA 1605
Db 1082 GAATTCCTAGAAAGAGCATCAAAGTAGACTAAAGCGCTTCTTAAACCGTGGAACTCGGGA 1141
QY 1606 AAGGATTTCTCAATGCCACACAGATTTCTGCCAGTGGCTTCCAGCAGATTAATGAAGTGT 1665
Db 1142 AAGGATTTCTCAATGCCACACAGATTTCTGCCAGTGGCTTCCAGCAGATTAATGAAGTGT 1201
QY 1666 CTCAACTGGCTTGGGGAAGAGACGACTGCTGAGAAACGACTACAAAAGAGCAAGAGT 1725
```

Db	1202	CTCAACTGGCTTGC	CGAGAAGACGACACTGCTGAGAACGACTACAAAGAACAAGGT	1261	
Qy	1726	ACATGGAAATACA	AGACACTAAAGAAGCCCTTTAGCTAGGACAAATTTGGAATTAGGAA	1785	
Db	1262	ACATGGAAATACA	AGACACTAAAGAAGCCCTTTAGCTAGGACAAATTTGGAATTAGGAA	1321	
Qy	1786	ATTCGTCCTCACA	GATTCGACTTCTTCCACATCGAATCAACCGGTGGAAGAGGTCTA	1845	
Db	1322	ATTTGTCCTCACA	GATTCGACTTCTTCCACATCGAATCAACCGGTGGAAGAGGTCTA	1381	
Qy	1846	ACCGTAAACTCTC	ATCGTCGCTGGTGAGACTCTTGCCCTCTTAGTGTAATTTTGGCTGT	1905	
Db	1382	ACCGTAAACTCTC	ATCGTCGCTGGTGAGACTCTTGCCCTCTTAGTGTAATTTTGGCTGT	1441	
Qy	1906	ACCATATAATTC	TGTTTCATGATGACTGTAACCTGTTTATGTCTATCGTTGGCGTCATAT	1965	
Db	1442	ACCATATAATTC	TGTTTCATGATGACTGTAACCTGTTTATGTCTATCGTTGGCGTCATAT	1501	
Qy	1966	AGTTTCGCTCTC	GTGTTTGGCATCCTGTGTATTATTCGTCAGGTTGCTTCAAACAAATG	2025	
Db	1502	AGTTTCGCTCTC	GTGTTTGGCATCCTGTGTATTATTCGTCAGGTTGCTTCAAACAAATG	1561	
Qy	2026	TTGTAAACAATT	GAAACAAATGGTATACAGATTTGTA	2061	
Db	1562	TTGTAAACAATT	GAAACAAATGGTATACAGATTTGTA	1597	
RESULT 10					
AR087506					
LOCUS	AR087506	1194 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 13 from patent US 5986082.				
ACCESSION	AR087506				
VERSION	AR087506.1 GI:10014269				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1194)				
AUTHORS	Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.				
TITLE	Altered forms of the NIM1 gene conferring disease resistance in plants				
JOURNAL	Patent: US 5986082-A 13 16-NOV-1999;				
FEATURES	Location/Qualifiers				
source	1..1194				
BASE COUNT	351 a	227 c	294 g	322 t	
ORIGIN	/organism="unknown"				
Query Match					
Best Local Similarity 56.5%; Score 1188.4; DB 6; Length 1194;					
Matches 1189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	466	TCGATTCGGTTG	TGACGTGTTTGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTA	525	
Db	2	TGGATTCCGGTT	TGACGTGTTTGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTA	61	
Qy	526	AAGGAGTTTCTG	AATCGCAGACGAGAATGCTGCCACGGCTTCCGCGCGCGCGGTG	585	
Db	62	ANGAGGTTTCGA	ATGCGCAGACGAGAATGCTGCCACGGCTTCCGCGCGCGCGGTG	121	
Qy	586	ATTTTCATGTTG	AGGTTTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTACTC	645	
Db	122	ATTTTCATGTTG	AGGTTTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTACTC	181	
Qy	646	TCTATCAGAGCA	CTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTA	705	
Db	182	TCTATCAGAGCA	CTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTA	241	
Qy	706	TACTCAAGCTTG	CTTAATATATGTTGTAAGCTTGATGAAGCTATTGGATAGATGTAAG	765	
Db	242	TACTCAAGCTTG	CTTAATATATGTTGTAAGCTTGATGAAGCTATTGGATAGATGTAAG	301	

Qy	766	AGATTATTGTC	CAAGTCTAATGTAGATATGGTTAGTCTTTGAAAAGTCATTGCCGGAAGAC	825	
Db	302	AGATTATTGTC	CAAGTCTAATGTAGATATGGTTAGTCTTTGAAAAGTCATTGCCGGAAGAC	361	
Qy	826	TTGTTAAAGAGA	TAAATGTATAGACGTTAAAGAGCTTTGGTTTGGAGGTACCTAAAGTAAAGA	885	
Db	362	TTGTTAAAGAGA	TAAATGTATAGACGTTAAAGAGCTTTGGTTTGGAGGTACCTAAAGTAAAGA	421	
Qy	886	AAACATGTC	TCGAATGTACATAAGGCACCTTGACTCGGATGATATTCAGTTAGTCAAGTTGC	945	
Db	422	AAACATGTC	TCGAATGTACATAAGGCACCTTGACTCGGATGATATTCAGTTAGTCAAGTTGC	481	
Qy	946	TTTTGAAAGAGA	GAGTACACACCAATCTAGATGATGCTGTGCTCTTCATTTTCGCTGTTCAT	1005	
Db	482	TTTTGAAAGAGA	GAGTACACACCAATCTAGATGATGCTGTGCTCTTCATTTTCGCTGTTCAT	541	
Qy	1006	ATTGCAATGT	GAAAGCCGCAACAGATCTTTTAAACCTTGATCTTCCGCTGATCTCAACCAT	1065	
Db	542	ATTGCAATGT	GAAAGCCGCAACAGATCTTTTAAACCTTGATCTTCCGCTGATCTCAACCAT	601	
Qy	1066	GGAATCCGAGG	GGATATACGGTCTTCATGTTGCTGCGATGCGGAAGGAGGCACAAATTGA	1125	
Db	602	GGAATCCGAGG	GGATATACGGTCTTCATGTTGCTGCGATGCGGAAGGAGGCACAAATTGA	661	
Qy	1126	TACTATCTCT	ATTGGAAGAGTGCAAGTGATCAGAGCAACTTTTGGAAAGGTAGAACCG	1185	
Db	662	TACTATCTCT	ATTGGAAGAGTGCAAGTGATCAGAGCAACTTTTGGAAAGGTAGAACCG	721	
Qy	1186	CACTCATGAT	GCACAAACGACCTATGCGGTTTGAATGTAATAATATCCGGAGCAAT	1245	
Db	722	CACTCATGAT	GCACAAACGACCTATGCGGTTTGAATGTAATAATATCCGGAGCAAT	781	
Qy	1246	GCAAGCATTCT	CTCAAAGCCGACTATGTTGTAAGAATACTAGACCAAGAAGCAACACGAG	1305	
Db	782	GCAAGCATTCT	CTCAAAGCCGACTATGTTGTAAGAATACTAGACCAAGAAGCAACACGAG	841	
Qy	1306	AACAAATTCCT	AGAGATGTTCTCCCTCTTTTGGCAGTGGCGCCGATGAATGAAGATGA	1365	
Db	842	AACAAATTCCT	AGAGATGTTCTCCCTCTTTTGGCAGTGGCGCCGATGAATGAAGATGA	901	
Qy	1366	CGCTGCTCAT	CTTGAAAATAGAGTTGCACTTGGCTCAACGCTTTTCCCAACGGAGCAC	1425	
Db	902	CGCTGCTCAT	CTTGAAAATAGAGTTGCACTTGGCTCAACGCTTTTCCCAACGGAGCAC	961	
Qy	1426	AAGCTGCAAT	GGAGATCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACGCTCG	1485	
Db	962	AAGCTGCAAT	GGAGATCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACGCTCG	1021	
Qy	1486	AGCCTGACCG	TCTACTGGTACGAAGAACATCACCGGGTGTAAAGATAGACACCTTTCA	1545	
Db	1022	AGCCTGACCG	TCTACTGGTACGAAGAACATCACCGGGTGTAAAGATAGACACCTTTCA	1081	
Qy	1546	GAACTCTAGA	AGAGCATCAAGTAGACTAAAAGCCCTTCTAAAACCGTGGAACTCGGGA	1605	
Db	1082	GAACTCTAGA	AGAGCATCAAGTAGACTAAAAGCCCTTCTAAAACCGTGGAACTCGGGA	1141	
Qy	1606	AACGATTCCT	CCCGCGCTGTTCCGCGAGTCTCGACAGATTAATGAACGT	1655	
Db	1142	AACGATTCCT	CCCGCGCTGTTCCGCGAGTCTCGACAGATTAATGAACGT	1191	
RESULT 11					
AR087507					
LOCUS	AR087507	786 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	Sequence 15 from patent US 5986082.				
ACCESSION	AR087507				
VERSION	AR087507.1 GI:10014270				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 786)				
AUTHORS	Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.				

TITLE		Altered forms of the NIM1 gene conferring disease resistance in plants																
JOURNAL		Patent: US 5986082-A 15 16-NOV-1999;																
FEATURES	source	Location/Qualifiers																
		1. .786																
BASE COUNT		221 a	136 c	200 g	229 t													
ORIGIN		/organism="unknown"																
Query Match		37.1%; Score 781.4; DB 6; Length 786;																
Best Local Similarity		99.9%; Pred. No. 4.3e-191;																
Matches 782; Conservative		0; Mismatches 1; Indels 0; Gaps 0;																
QY	399	GACTCCAAACACCGCCGCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAA	458															
Db	4	GACTCCAAACACCGCCGCGTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAA	63															
QY	459	GTCGGTTTCGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCG	518															
Db	64	GTCGGTTTCGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCG	123															
QY	519	CCGCTTAAAGGAGTTTCTGAATCGCCACAGCAGAAATGCTGCCACGTGGCTTCCCGCCG	578															
Db	124	CCGCTTAAAGGAGTTTCTGAATCGCCACAGCAGAAATGCTGCCACGTGGCTTCCCGCCG	183															
QY	579	CGCGTGGAATTCATGTTGGAGGTTCTCTATTTCGCTTTCATCTTCAAGATCCCTGAATTA	638															
Db	184	CGCGTGGAATTCATGTTGGAGGTTCTCTATTTCGCTTTCATCTTCAAGATCCCTGAATTA	243															
QY	639	ATTACTCTATCAGAGCACCATTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACA	698															
Db	244	ATTACTCTATCAGAGCACCATTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACA	303															
QY	699	TTGGTTATACTCAAGCTTCCTAATATATGTGTTAAAGCTTCTATGAAGCTATTGGATAGA	758															
Db	304	TTGGTTATACTCAAGCTTCCTAATATATGTGTTAAAGCTTCTATGAAGCTATTGGATAGA	363															
QY	759	TGTAAGAGATTATTGTCAAGTCTAATGTAGATATGTTAGTCTTGAAAAGTCATTGCCG	818															
Db	364	TGTAAGAGATTATTGTCAAGTCTAATGTAGATATGTTAGTCTTGAAAAGTCATTGCCG	423															
QY	819	GAAGAGCTTGTAAAGAGATAATTGTAGACGTAAGAGCTTGGTTGGAGGTACCTAAA	878															
Db	424	GAAGAGCTTGTAAAGAGATAATTGTAGACGTAAGAGCTTGGTTGGAGGTACCTAAA	483															
QY	879	GTAAGAAACATGCTCTGCAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTC	938															
Db	484	GTAAGAAACATGCTCTGCAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTC	543															
QY	939	AAGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGGTGCTCTTCATTTCGCT	998															
Db	544	AAGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGGTGCTCTTCATTTCGCT	603															
QY	999	GTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTTGCGGATGTC	1058															
Db	604	GTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTTGCGGATGTC	663															
QY	1059	AACCATAGGAATCCGAGGGGATATACGGTTCATGTTGCTGGATCGGAAGGAGGCCA	1118															
Db	664	AACCATAGGAATCCGAGGGGATATACGGTTCATGTTGCTGGATCGGAAGGAGGCCA	723															
QY	1119	CAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGT	1178															
Db	724	CAATTGATACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGT	783															
QY	1179	AGA 1181																
Db	784	TGA 786																
RESULT 12																		
ATF20B18																		
LOCUS		ATF20B18	104738 bp	DNA	linear	PLN	24-MAR-1999											

Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project).	DEFINITION
AL049483	ACCESSION
AL049483.1 GI:4538918	VERSION
thale cress.	KEYWORDS
Arabidopsis thaliana	SOURCE
Arabidopsis thaliana	ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 104738)	REFERENCE
Bevan,M., Rose,M., Hempel,S., Entian,K.-D., Hoheisel,J., Mewes,H.W., Mayer,K.F.X. and Schueller,C. 2 (bases 1 to 104738)	AUTHORS
EU Arabidopsis sequencing project.	JOURNAL
Submitted (18-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schueller@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk	REFERENCE
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can be viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.	AUTHORS
Location/Qualifiers	FEATURES
1..104738	source
/organism="Arabidopsis thaliana"	
/variety="Columbia"	
/db_xref="taxon:3702"	
/chromosome="4"	
86..261	exon
/gene="F20B18.10"	
/number=1	
Join(86..261,380..514,606..708,761..896,1006..1175)	CDS
/gene="F20B18.10"	
/note="similarity to Pennisetum ciliare possible	
apospory-associated mRNA clone pSUB C, PID:g549984"	
/codon_start=1	
/product="possible apospory-associated like	
protein(fragment)"	
/protein_id="CAB39655.1"	
/db_xref="GI:4538919"	
/translation="MFMEYQYSNTGPLPSHGVRORFEVETKPPPLPSLTAHVDL	
IVRSNEDLKIWPHKFEYRLRLVALHGCDJLILSRVKNTDKPFTFALHPYFVSN	
ISELHVGLHNDLYDOQKNTFTDHEKVITFNAOSTTKKTKTLQKLDRLXLTSP	
QLRLVDHKKKTIIVVHKRGQVDVAVNPNWDKKVSDGLVEDYKREVTVEASAARKPT	
NPGEKWKGLIHVSVPVSNRKA"	
86..1175	gene
/gene="F20B18.10"	
262..379	intron
/gene="F20B18.10"	
/number=1	
380..514	exon
/gene="F20B18.10"	
/number=2	
515..605	intron
/gene="F20B18.10"	
/number=2	
606..708	exon
/gene="F20B18.10"	
/number=3	
709..760	intron
/gene="F20B18.10"	
/number=3	
761..896	exon
/gene="F20B18.10"	
/number=4	
897..1005	intron
/gene="F20B18.10"	
/number=4	
1006..1175	exon

DEFINITION	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project).
ACCESSION	AL049483
VERSION	AL049483.1
KEYWORDS	GI:4538918
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 104738)
AUTHORS	Bevan,M., Rose,M., Hempel,S., Entian,K.-D., Hoheisel,J., Mewes,H.W., Mayer,K.F.X. and Schueller,C.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 104738)
AUTHORS	EU Arabidopsis sequencing,project.
TITLE	Direct Submission
JOURNAL	Submitted (18-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schueller@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can be viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/ .
FEATURES	Location/Qualifiers
source	1..104738
	/organism="Arabidopsis thaliana"
	/variety="Columbia"
	/db_xref="taxon:3702"
	/chromosome="4"
exon	86..261
	/gene="F20B18.10"
	/number=1
CDS	join(86..261,380..514,606..708,761..896,1006..1175)
	/gene="F20B18.10"
	/note="similarity to Pennisetum ciliare possible
	apospory-associated mRNA clone pSUB C, FID:9549984"
	/codon_start=1
	/product="possible apospory-associated like
	protein(fragment)"
	/protein_id="CAB39655.1"
	/db_xref="GI:4538919"
	/translation="MFEMEYQYSNTGPLPSHGVRQRFWEVETKPPPLPSLTAHVDL
	IVRSSNEDLKIWPHKFEYRLKVALGHDGDLTISRKNTDTKPFNTFALHPIFAVSN
	ISEIHVEGLHLDYLDQOKNRTFTDHEKVTITFNAQSITKKKHTLQKKDLRLYSTPD
	QLRIVDHKKKTIYVHKEGQVDVAVNPNWDKVSIDLGVEDYKRFVTVEESAARQITV
	NPGEWKGIILHVSVPVSNRKA"
gene	86..1175
	/gene="F20B18.10"
intron	262..379
	/gene="F20B18.10"
	/number=1
exon	380..514
	/gene="F20B18.10"
	/number=2
intron	515..605
	/gene="F20B18.10"
	/number=2
exon	606..708
	/gene="F20B18.10"
	/number=3
intron	709..760
	/gene="F20B18.10"
	/number=3
exon	761..896
	/gene="F20B18.10"
	/number=4
intron	897..1005
	/gene="F20B18.10"
	/number=4
exon	1006..1175

```

/gene="F20B18.10"
/number=5
1942..2872
/gene="F20B18.20"
join(1942..2007,2093..2210,2286..2584,2681..2872)
/gene="F20B18.20"
/notes="similarity to nitrogen fixation protein nifu -
Anabaena sp., P1r2:D34443"
/codon_start=1
/product="nitrogen fixation like protein"
/protein_id="CAB39656.1"
/db_xref="GI:4538920"
/translation="MNISSLTAERNPNFRSSLLSKNAISDTLGVSKKSTFLRGQFQ
LWVVKLAGACGCPSSMTLKMIESRLRDKIPFIMSVQFLESETGGLELNDENIE
KVLSRLRYLSTGGGGLLEIDGVVYKVLRTGPAAGVTVRVVALTKLRETIPIG
AVQLLE"
1942..2007
/gene="F20B18.20"
/number=1
2008..2092
/gene="F20B18.20"
/number=1
2093..2210
/gene="F20B18.20"
/number=2
2211..2285
/gene="F20B18.20"
/number=2
2286..2584
/gene="F20B18.20"
/number=3
2585..2680
/gene="F20B18.20"
/number=3
2681..2872
/gene="F20B18.20"
/number=4
3253..4619
/gene="F20B18.30"
join(3253..3313,3471..4146,4259..4619)
/gene="F20B18.30"
/notes="similarity to other hypothetical proteins
Arabidopsis thaliana"
/codon_start=1
/product="putative protein"
/protein_id="CAB39657.1"
/db_xref="GI:4538921"
/translation="MSKLIIRIFKPSVCKNLFVPPFLLIDYILNNPNSSDGRVTT
NYGNEKVLINKDLKEEVCDAMTVGFRDGLRVELCGNHDVCSPFIYKPTDPEI
EDLTVDPLPTGSIQSLVMSLLPKRDKNWVVKLGSLSCMRPFGRKWINIQT
KPNINPSSIMFSKKEKKFYVPTGGNLCYLDPHSDDDLIDFVEFDLPKSVF
QELADVSCSRDHLVESPTQLFLVWKYGDELDIDNTTLYNVTYKFMVPEKEGES
CVYTKKMIYTDIGDLCIFVGHSEAFQVPASSSPGLPNCIYFVGINFGVYDLITKTC
TMFTFKDNDPLRKLFFPYWPPPPSPFLAPN"
3253..3313
/gene="F20B18.30"
/number=1
3314..3470
/gene="F20B18.30"
/number=1
3471..4146
/gene="F20B18.30"
/number=2
4147..4258
/gene="F20B18.30"
/number=2
4259..4619
/gene="F20B18.30"
/number=3
5155..5183
/gene="F20B18.40"
/number=1
```

```

gene
CDS
5155..7171
/gene="F20B18.40"
join(5155..5183,5229..5454,6046..6773,6850..7171)
/notes="similarity to other hypothetical proteins
Arabidopsis thaliana"
/codon_start=1
/product="putative protein"
/protein_id="CAB39658.1"
/db_xref="GI:4538922"
/translation="MAPHOTQERYGCHNLNRHNVETLVHMASQPMVFRAPESWEEK
YVITIDGDLGICFLGHSFAFCIQASSGSLTASILWALTLSHKSQVPMFSSKPTYP
YLLIDHLTKTTHSNDQYIYDKYIEKNLVIRDOGLAEEVREVMTVGSHDDWRVH
LEKESDSTSLMNSVNTSPVKHQPLPSSNCRIONVAISNVSDIKKEDLVVAVKFF
GSDVLSCKPFSOSSSEMINTSVSPKFKLSLTSVSPSGHTYLYLIDLHF
DEDDVRPSSYLYFREDPLRLRYIKMDLEDYIWRFTDHLAELPSGEHFLVKWFFKDV
MNVGKIKTQKTDGFKFVRTICGHLTNTODIGDLCIFLGHGEAYCVPASSSPGLRPN
IYVGCNFGVHDITADTTNFYTHSNVPLRSTFEFFWPLPLS"
5184..5228
/gene="F20B18.40"
/number=1
5229..5454
/gene="F20B18.40"
/number=2
5455..6045
/gene="F20B18.40"
/number=2
6046..6773
/gene="F20B18.40"
/number=3
6774..6849
/gene="F20B18.40"
/number=3
6850..7171
/gene="F20B18.40"
/number=4
7172..10478
/gene="F20B18.50"
complement(7570..7980)
/gene="F20B18.50"
/number=1
complement(join(7570..7980,8077..8210,8292..8367,
8449..8652,8754..8831,9062..9127,9216..9332,9408..9521,
9598..9725,9822..9960,10052..10149,10227..10296,
10389..10478))
/gene="F20B18.50"
complement(join(7570..7980,8077..8210,8292..8367,
8449..8652,8754..8831,9062..9127,9216..9332,9408..9521,
9598..9725,9822..9960,10052..10149,10227..10296,
10389..10478))
/gene="F20B18.50"
/notes="similarity to synapse-enriched clathrin adaptor
protein LAP - Drosophila melanogaster, PID:g4160434
```

```

Query Match 32.6%; Score 686.4; DB 8; Length 104738;
Best Local Similarity 64.8%; Pred. No. 2.8e-166;
Matches 1304; Conservative 0; Mismatches 426; Indels 282; Gaps 8;

Qy 98 CACCACCATTCATGGATCGCGGATCTCTTGAATCAGCAGCAGCTAGTTTCGTCGCTAC 157
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74243 CACCACCATTCATGGATCTCTGATTCATGAGTTCAGCAACACAGCGGCAATAGCTT 74302

Qy 158 CGATAACACCGACTCTCTATTTGTTTATCTGGCGCGCAACAGTACTACCGGACTGA 217
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74303 CTTCCGCGCGAGTCACTCTCTTGATTTATCCGACG-----AATTTCTACGCCACGGA 74356

Qy 218 TGTATCTGCTCTGCAATTCCTCTCCACAGCTTCGATCCGCTCTTTCAGTCGCGGATGA 277
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74357 GGTATCAGCTCTTAAACTTCCTGCTAACTGCCTCAGTCTGTTCGACTCGCGGAGAC 74416

Qy 278 TTTCTACAGCGACCTAAGCTTGTCTCCGACGCGCGGGAAGTTTCTTTCACCCGGTG 337
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74417 GTTCTACAGCATGCTAAGTAGTTCTCGCGCGCGGGAAGTTTCTTTCACCCGGTG 74476
```


REFERENCE	4 (bases 1 to 196286)	
AUTHORS	EU Arabidopsis sequencing project.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lencke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevand@brc.ac.uk	
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV63 at the 5' end and an overlap with ATCHRIV65 at the 3' end.	
FEATURES	Location/Qualifiers	
source	1. 196286	
	/organism="Arabidopsis thaliana"	
	/variety="Columbia"	
	/db_xref="taxon:3702"	
	/chromosome="4"	
gene	6687. .8444	
exon	/gene="AT4g25770"	
	complement(6687. .6833)	
	/gene="AT4g25770"	
	/number=1	
gene	complement(join(6687. 6833,6920. .7036,7083. .7163,7278. .7370,7494. .7733,7782. .7882,7945. .8042,8134. .8444))	
	/gene="AT4g25770"	
CDS	complement(join(6687. .6833,6920. .7036,7083. .7163,7278. .7370,7494. .7733,7782. .7882,7945. .8042,8134. .8444))	
	/gene="AT4g25770"	
	/note="similarity to hypothetical protein T2711.6 - Arabidopsis thaliana, PIR2:T00623"	
	/codon_start=1	
	/product="putative protein"	
	/protein_id="CAB79432.1"	
	/db_xref="GI:7269428"	
	/translation="MIASFRRQISIPDLIPSSPRFLPPSQNFRRLYLQFPAQPN LCOMENRIGIGCFANRKRLETTEDNGGDFEDADYMSAEKPDHLVVMVGIV GSAADWYAAQFVKPKPDVLRACFLAYRYCGSESNATLTEDGVRKMGRLANE VFGCIVVSSVGVVKKRSGLKKISFVAHSLGLGVARYAGKLYEQGEVDSLDSPK EKSARGIEAGLEPMNFTFATPHLGRGHRQFPILCGLPFLERTASQTAHLAARGT KHLFLIDMLITSSYDLNARSALNAFRRVAVANRLSMVDFYFLQEFALNEXAMVGW RLTSSIRRNELPKPNULLATDPNPHIVVYVGRGVNDGSCQSTSTVTVTQDTLEGFAL FLT"	
intron	complement(6834. .6919)	
	/gene="AT4g25770"	
exon	/number=1	
	complement(6920. .7036)	
	/gene="AT4g25770"	
intron	/number=2	
	complement(7037. .7082)	
	/gene="AT4g25770"	
exon	/number=2	
	complement(7083. .7163)	
	/gene="AT4g25770"	
intron	/number=3	
	complement(7164. .7277)	
	/gene="AT4g25770"	
exon	/number=3	
	complement(7278. .7370)	
	/gene="AT4g25770"	
intron	/number=4	
	complement(7371. .7493)	
	/gene="AT4g25770"	
exon	/number=4	
	complement(7494. .7733)	
	/gene="AT4g25770"	
intron	/number=5	
	complement(7734. .7781)	
	/gene="AT4g25770"	
exon	/number=5	
	complement(7782. .7882)	

	intron	/gene="AT4g25770"	
		number=6	
		complement(7883. .7944)	
		/gene="AT4g25770"	
	exon	number=6	
		complement(7945. .8042)	
		/gene="AT4g25770"	
		number=7	
	intron	complement(8043. .8133)	
		/gene="AT4g25770"	
		number=7	
	exon	complement(8134. .8444)	
		/gene="AT4g25770"	
		number=8	
	CDS	9569. .10141	
		/gene="AT4g25780"	
		/note="strong similarity to gene PR-1 protein - Medicago truncatula, PIR2:S47171	
		Contains Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	
		signatures AA147-157; Extracellular proteins	
		SCP/Tpx-1/Ag5/PR-1/Sc7 signatures AA173-184	
		contains EST gb:Z36548, AA586201, AA712838, AA712715"	
		/codon_start=1	
		/product="putative pathogenesis-related protein"	
		/protein_id="CAB79433.1"	
		/db_xref="GI:7269429"	
		/translation="MSSSVLRVILLGALNVVSVLSITNSLITKSATLGOVFRICKNL	
		CPGCDHDSIQFELRHNLVRAARFEPPLIWRRLQNYAQGWANORRGDCALRHVSNGE	
		FNLGNIYGYGANNSPADAVVAWASEKRFYHYGSNTCDAGQMGCHYTQIVMKSTRRV	
		GCARVCDNGGIFMTCNDYPPGNYIGQRPY"	
	exon	9569. .10141	
		/gene="AT4g25780"	
		number=1	
	gene	9569. .10141	
		/gene="AT4g25780"	
	exon	complement(10710. .11074)	
		/gene="AT4g25790"	
		number=1	
	gene	10710. .11752	
		/gene="AT4g25790"	
	gene	complement(join(10710. .11074,11485. .11752))	
		/gene="AT4g25790"	
	CDS	complement(join(10710. .11074,11485. .11752))	
		/gene="AT4g25790"	
		/note="strong similarity to gene PR-1 protein - Medicago truncatula, PIR2:S47171	
		Contains Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	
		signatures AA166-176; Extracellular proteins	
		SCP/Tpx-1/Ag5/PR-1/Sc7 signatures AA193-204	
		contains EST gb:AA712715, N65358"	
		/codon_start=1	
		/product="putative pathogenesis-related protein"	
		/protein_id="CAB79434.1"	
		/db_xref="GI:7269430"	
		/translation="MATTTSQAIFAIALFLVAIOAHVADYRHRPQRPITPSPPPY	
		VAKPQLPFPSPKPIYQPPYQPTGSFEQQLDPHNTVGGGLGPLVWVDVKLAS	
		YATWANQRIDCSLTHSGPYGLENFWSGSDFTSTFAVESKTFEAKSYNHNMTNCE	
		GDGMCGHYTQIWRTRRLRGCAVVCENGAVFITCNIDYPPGNYVGEKPY"	
	intron	complement(11075. .11484)	
		/gene="AT4g25790"	
		number=1	
	exon	complement(11485. .11752)	
		/gene="AT4g25790"	
		number=2	
	gene	13985. .16227	
		/gene="AT4g25800"	
	CDS	join(13985. .14010,14239. .14669,14761. .14921,15016. .15219,15390. .15595,15645. .16227)	
		/gene="AT4g25800"	
		/note="EST GB:F14385 in 5' untranslated region	
		strong similarity to calmodulin-binding protein (TCB60) -	
		Nicotianatabacum, PID:g1698548	
		contains EST gb:F14386, F14385, N96168, N96141"	


```
/codon_start=1
/product="putative calmodulin-binding protein"
/protein_id="CAB79435.1"
/db_xref="gi:7269431"
/translation="MNQFCLLVRLSLPLFTGGRVVEGQATIHVVLIDANTGRPVTVG
PEASLUKEVVVLGGDFNDEDDTQEEFESHVYKEREKRLPLITGLDFVYLKEGVGT
LGEIVTDNSWIRSRKFRGLRGVSGYCDGIRIREAKTEAFSVKDRHGLYKKHYP
ALNDVWRLEKIGKDGAFHKRLTAAGIVTVEGFLURLVRDSTKLRLILGSGMSNMWD
LLVHAKTCLVSGKLYIVYEDSRVGVWNNIYELSGLLITEQYLSADLSLSQKVY
VDGLVKAYENNNOVVEGESLLNLNQPERLDISQDFVPTALASYSTVPLSOPPEFA
LEGHQISPLFYSTSIPTAGYNQTLITALPHNPQAFDFVQQDOFQIGIQPQQTINIE
NENVRILVGLPFGSGTGYQDIKSSADOENLPEDWNLSENDFFSEERIQTSHDL
LANEDMOQLFSGMGKGEDGFTFSPMONTMMQGYDEEGRSGRAVVGWLKVRAA
NRWGFTRKRAAERRAQIVLHLDNNDGK"
13985..14010
/feature="AT4g25800"
exon
/number=1
intron
14011..14238
/feature="AT4g25800"
/number=1
exon
14239..14669
/feature="AT4g25800"
/number=2
intron
14670..14760
/feature="AT4g25800"
/number=2
exon
14761..14921
/feature="AT4g25800"
/number=3
intron
14922..15015
/feature="AT4g25800"
/number=3
```

```
Query Match 32.6%; Score 686.4; DB 8; Length 196286;
Best Local Similarity 64.8%; Pred. No. 2.9e 166;
Matches 1304; Conservative 0; Mismatches 426; Indels 282; Gaps 8;

QY 98 CACCACCATGATGATTCGGCGATTCCTATCAATCAGCAGCAGTCTGTCGCTAC 157
Db 124928 CACCACCGGTAGATTCCTGATTCATACAGGTTACAGACACAGCGGCAATGCTT 124987

QY 158 CGATAACACCGACTCCTCTATTGTTTATCTGGCGCGCGAACAAGTACTACCGACCTGA 217
Db 124988 CTTCCGCCCGCGAGTCACTCTGTTGATTATCCGACGG-----AATTTCTCAGCCACGGA 125041

QY 218 TGTATCTGCTCTGCAATTCCTCCACAGCTTCGAATCCGCTTTGACTCCGCGGATGA 277
Db 125042 GGTATCAGCTCTTAACTTCCTGCTAACTCGCTCGAGTCTGTTTTCGACTCGCGGAGAC 125101

QY 278 TTCTACAGCAGCTAAAGCTTGTCTCTCCGAGCGCGGGAAGTTCCTTTCCACCGGTG 337
Db 125102 GTTCTACAGCATGCTAAGTAGTTCTCGCGCGCGCGGGAAGTTCCTTTTACCGGTG 125161

QY 338 CGTTTGTTCAGCGAAGCTCTTCTTCAAGAGCGCTTTAGCCGCGCGTAAAGAGGAGAA 397
Db 125162 TATTCTTTCCGCGAAGTTCCTGCTCTTCAAAAGCGCTTTAGCCACCGTGAAGGAACAAA 125221

QY 398 AGACTCCAAACAACCGCGCGGTGAAGCTCGAGCTTAAGAGATTGCCAAGGATTACGA 457
Db 125222 ATCCTCCA-----CCACCGTGAAGCTCCAGCTGAAGAGATCCGAGAGATTACGA 125272

QY 458 AGTCGGTTTCGATTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGCTGAGACC 517
Db 125273 AGTCGGCTTTCGACTCGGTTGTGGCGGTTTGGCGTATGTTTACAGCGCAGAGTGAGTC 125332

QY 518 GCCGCCTAAAGAGATTCTGAATCCGAGAGCAAAATGTCGCCACGTGGCTGCGCGCC 577
Db 125333 CCCGCCGAAGGGAGCTTCTGCTCGCTAGCAGCAATTTGTCACGCTGGCTTGCCTG 125392

QY 578 GCGCGTGATTCATGTTGGAGGTTCTCTATTTCGGCTTTCATCTTCAAGATCCCTGAATT 637
Db 125393 AAGGTGGATTTCATGTTGGAGGTTCTTATCTCTCTTCGTTTTCAGGATTCAAGAATT 125452
```

```
QY 638 AATTACTCTCTA----- 649
Db 125453 AGTTACTCTGTATGAGGTAAACAACAATCCACTAAATTCATTTGACTATAACATCATC 125512
QY 650 -----TCAGAGGCACATTATTGGACGTTTGTAGACAAAGTTCTTTA 687
Db 125513 TTAAGTCTCCTCTCTTTTCATTTTCAGAGGCAGTCTCTGGAAATGTAGACAAAGTTGTAG 125572
QY 688 TAGAGGACACATTTGGTTTATCTCAAGCTTCTCTAATATATCTGTTAAAGCTTGTATGAAGC 747
Db 125573 TCGAAGACATCTTTGGTTTATATTCAGCTTCTATCTATGTGTACAAATACAAAGAAGC 125632
QY 748 TATTGGATAGATGTAAGAGACATTATCTCAAGCTCTAATGTAGATATGTTAGTCTTGAAG 807
Db 125633 TTTTGGATAGATGATAGAAATTTATCGTGAAGTCTGATATAGAACTAGTTAGTCTTTGAGA 125692
QY 808 AGTCATTTGCCGGAAGAGCTTTGTTAAAGAGATAATTATAGACGCTAAAGACACTTGGTTTGG 867
Db 125693 AGTCATTTACCTCAACACATTTTCAAGCAATCATAGACATCCCGGAAGCGCTCTGTCTAG 125752
QY 868 AGGTACCTAAAGTAAGAAACATGTCTCGAATGTACATAAGGCACCTTGACTCGGATGATA 927
Db 125753 AGGCACCTAACTAGAAAGCATGTCTCAAGAACATATACAAAGCGCTAGACTCAGATGATG 125812
QY 928 TTGAGTTAGTCAAGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTGCTC 987
Db 125813 TTGAGCTTGTCAAGATGCTTTTGTCTAGAGGACACACCAATCTCGATGAGCGGTATGCTC 125872
QY 988 TTCATTTTCGCTGTTGTCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTTGATC 1047
Db 125873 TTCATTTTGTCTATCGCTCACTCGCTGTGAAGACCGGTATGATCTCCTCGACCTTGAGC 125932
QY 1048 TTGCCGATGTCACCATAGGAATCCGAGGGATATACGGTGTCTCATGTTGCTGCGATGC 1107
Db 125933 TTCCGGATGTTAACTTTAGAAATCCGAGGGATACACTGTGCTTCATGTTGCTGCGATGC 125992
QY 1108 GGAAGGAGCCACAAATGTACTATCTCTATTGCAAAAAGTGCACATGATCAGAACAA 1167
Db 125993 GGAAGGAGCCGAGTTGATATATCTTTGTTAATGAAGGGGCAAAATATTTTAGACACAA 126052
QY 1168 CTTTGAAGTAGAACCGCCTCATGATCGCAAAACCAAGCCACTATGGGGTTTGAATGTA 1227
Db 126053 CATTTGATGTTAGAACCGCTTTAGTATGTTAAACGACTCCTAAAGCGGATGACTACA 126112
QY 1228 ATATATCCCGAGCAATGCAAGCATCTCTCAAGGCGGCACTATGTGTAGAAATACTAG 1287
Db 126113 AAACTAGTAGGAGGAGCGGTACGCTCTCTGAAAGGCGGATTTATGCATAGAGGTACTTG 126172
QY 1288 AGCAAGAAGACAAACGAGAACAAAT---TCCTAGAGATGTTCCCTCCCTCTTTTGCAGTGG 1344
Db 126173 AGCATGAACAAAACCTAGAAATATTTGTGCGCTATAGAGGCTTCACHTTCTCTTCCAGTAA 126232
QY 1345 CGGCCGATGAATTTGAAGATGACGCTGCTCGATCTTGAATA----- 1384
Db 126233 CTCGAGGAGGTTGAGGATGAGGTGCTCTATTATGAAAACCGGAGGTATGCTTTCTTCTCT 126292
QY 1385 ----- 1384
Db 126293 TCACCTGAATATCGAATTTCCGGGTAGGAAAATAGTGGAACTAATGATAACGATGCTCTA 126352
QY 1385 -----TAGAGTTGCACCTTGCTCAACGCTCTTTTCCAAACGGAAGACACAAGCTGCAATGGAG 1439
Db 126353 TACTTTTCAGTTGCACCTTGCTCGACTTCTCTTTCCAGTGGAACTGAAACTGTACAGGT 126412
QY 1440 ATCCGCCAAATGAAGGAAACATGTGATTTCAATAGTACTAGCCTCGAGCCTGACCGCTCTC 1499
Db 126413 ATTGCCAAAATGGAGAAACATGCGAGTTTACAGCTTCTAGTCTCGAGCCTGATCATCAC 126472
QY 1500 ACTGGTACGAAGACATCACCAGGAGTGAAGATAGACACTTTTCAGAAATCCTAGAGAG 1559
Db 126473 ATTTGGTGAAGAGCGGACATCACTAGACCTTAAATATGTCGCCCGTTCCAAATCCATGAGA 126532
QY 1560 CATCAAAGTAGACTAAAGCGCTTTTCTAAACCC----- 1592
```



```
Db 1160 TTCTTCAGAGGCAATTCACAGGACACAGGAGAGATGACAGTCCGGGCTCTCGT 1219
QY 1804 CGACTTCTTCACATCGAAATCAACCGGTGGAAGAGG 1841
Db 1220 CGTGTATCATGACATCGATCGGGGCCATTCGACCAAG 1257

RESULT 15
AX351145
LOCUS AX351145 1668 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 19 from Patent WO0166755.
ACCESSION AX351145
VERSION AX351145.1 GI:18616498
KEYWORDS
SOURCE bread wheat.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (sites)
Wang,H.X., Salmeron,J.M., Willits,M.G. and Lawton,K.A.
Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 19 13-SEP-2001;
SYNGENTA Participations AG (CH)
FEATURES
Location/Qualifiers
1..1668
/organism="Triticum aestivum"
/db_xref="taxon:4565"
451..1668
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22848.1"
/db_xref="GI:18616498"
/translation="MPFFSMQRLHDLFDKVEVDNLPLILSVANLKNKSCVKLPERCM
EMVVRNLDMITLEKALPDQVIKQITDLRITGLASPEDNGFPNKHVRILRALDSD
VELVRMLTGQTNLDADPALHYAVEHCDISKITTELDLADVNLNRPRGTVLHIA
AKRRDPKIVVSLTKGAPSPDFDGRKAVQISKRLLKHGDFEGNTEGKPSPNKLC
IEILEAERDLPOLGASLSLALAGDLRGKLLYLENVALARIMPPIEARVAMDIQ
VDGLFTLGSSNPLEITVDLNTSFMKEEHLARMLRSKVELGKRFPPRCNS
VLKIMDDPELASFGLDASSERKRFRHDLQTLKAFSEDEKFEFRNRTTLSSSSST
SVIRNLNAGTRR"
BASE COUNT 470 a 328 c 360 g 510 t
ORIGIN

Query Match 15.0%; Score 314.6; DB 6; Length 1668;
Best Local Similarity 57.3%; Pred. No. 2.6e-70;
Matches 688; Conservative 0; Mismatches 474; Indels 39; Gaps 5;

QY 651 CAGAGGCACATTATGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATATC 710
Db 469 CAGCGCATCTCCTTGATTTCCITGTATAAGTTCAAGTGGATAACCTTCGGTTGATCTTA 528
QY 711 AAGCTTGCTATATATGTGTTAAGCTTGTATGAAGCTATTGGATAGATGAAGAGATT 770
Db 529 TCTGTGCAAACTTATGCAACAAATCTTGGCTGAAACTGTTCGAGAGATGCATGGAGATG 588
QY 771 ATTGCTCAAGTCTAATGTAGATATGGTTAGTCTTCAAAAGTCATTGCCGGNAGAGCTTGT 830
Db 589 GTAGTCGGGTCAAACTTGTACATGATTACTCTAGAGAAAGCATTTGGCTCAAGATGTCATC 648
QY 831 AAAGAGATAATTATAGACATAAGAGCTTGGTTTGGAGGTACCTAAAG----- 879
Db 649 AAGCAAAATTACTGATTTACGGATAAATCTTTGGATTAGCTTACCACCGAAGACAATGCTTT 708
QY 880 -TAAGAAACATGCTCGAATGTACATAAGGCACTTGACTCGGATGATATGAGTTAGTC 938
Db 709 CCTAACAAACACGCTAAGAAGGATACAGAGCACTTGAATTCGTGATGATGGAGCTTGC 768
QY 939 AAGTTGCTTTTGAAGAGGATCACCAATCTAGATGATCGGTGCTCTTCAATTCGCT 998
Db 769 AGGATGCTGCTACAGNAGGCGACACTAACCTTGTATGATGCATTTGCTGCACTATGCT 828
```

```
QY 999 GTTGCATATTCGAATGTGAAGACCGCAACAGATCTTTTTAAAACCTTGATCTTCCCGATGTC 1058
Db 829 GTAGAACACTGTGACTCAAAAATTTACAACAGAAGCTTCTGGACATCGCACTTCCGGATGTT 888
QY 1059 AACCATAGGAATCCGAGGGATATACGGTCTTTCATCTTTCCTGCGATCGGAAGAGGACA 1118
Db 889 AATCTCAGAAACCAAGAGGTTATCTGTCTTTCACATCCCGCTTAAGCGGAGAGATCCT 948
QY 1119 CAATTCATATCTCTATTGGAAGGTCGAAGTGCATCAGAAGCAACTTTTGAAGGT 1178
Db 949 AAAATCGTTGTCTCCCTTTTAAACAAAGTCCCGGCCCTTCAGATTTTACATTTGATGGA 1008
QY 1179 AAGACCGCACTCATGATCCGAAACAAAGCCACTATGCGCGGTTGAATGTAATATATCCCG 1238
Db 1009 AGAAAAGCAGATTCAAATCTCAAAGAGACTCACAAAACATGGTGATATTTTGGGATACT 1068
QY 1239 GAGCAATGCAAGCATCTCTCAAAAGCCGCACTATGTGTAGAAATACTAGACGAAGAAGAC 1298
Db 1069 GAGAAAGGAAGCCGCTCCCAATGATAAATATGCAATGAGATATTGGAGCAAGCTGAA 1128
QY 1299 AAGCAGAAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGCCGATGAATTG 1358
Db 1129 AGAAGGATCCCAACTTGGAGAAGCATCACTTTCTCTTTCATTTGCTGCTGCTGCTGCTT 1188
QY 1359 AAGATCAGCTGCTCGATCTTGAAATATAGATTGCACTTGTCTCAAGCTCTTTTCCAAAG 1418
Db 1189 CGTGAAGATTACTGTACCTTGAAAACCGAGTTGCTTTGGCAAGGATATATGTTTCCAATT 1248
QY 1419 GAAGCAACAAGCTGCAATGAGATCGCGAAATCAAGGGAACATGTGAGTTCATGTGACT 1478
Db 1249 GAGGCAAGAGTAGCAATGACATGCTCAAGTGGATGGTACTTTTGAATT-----T 1299
QY 1479 AGCCTCGAGCCTGACCGTCTCACTGGTAGAAGAGAACAATCACCGGTTGTAAGATAGCA 1538
Db 1300 ACCCTTGGTCTAGTACAAATCCACCTCTGGAGATAACAACCGTTGATCTGAATGATACT 1359
QY 1539 CTTTTCAGATCCTAGAACAGCATCAAGTAGACTAAAAGCCGCTTCTTAAACCGTGGAA 1598
Db 1360 TCTTTCAAAATGAAGGAGGAAACACTAGCTCGGATGAGAGCCCTCTCCAAAACAGTTGAA 1419
QY 1599 CTCGGAAACGATTCTTCCCGCGCTGTTTGGCAGTCTCGACAGATTTATGAATGTGAG 1658
Db 1420 CTCGGCAACGTTTCTTCCACGCTGTTCAATGTGCTGGCAAGATCATGACCATGA- 1478
QY 1659 GACTTGACTCAACTGGCTTGGGAGAGACGACACTGTGTGAGAAACGACTACAAAAGAG 1718
Db 1479 -----ACCTGAGCTGGCTTCCCTCGGAGAGATGC-----ATCCTCCGAGAGAG 1524
QY 1719 CAAAGGTACATGGAATACAAGAGACACTTAAAGAAGGCTTTAGTGAGGACAAATTTGGA 1778
Db 1525 AGGAGGTTTCAGCACTGCAAGTACGCTTCTGAAGGCGCTTCAGCGAGGACAAAGGAGAG 1584
QY 1779 TTAGGAAATTCGTCCTGACAGATTGCACTTCTTCCACATCGAAATCAACCGGTGGAAG 1838
Db 1585 TTTAAACAGAACGAC---AACCCCTTTCATCTCGTTCATCGTCGACGCTCCACTGTAGCAAGG 1641
QY 1839 A 1839
Db 1642 A 1642
```

Search completed: October 8, 2002, 00:34:40

Job time : 3196.57 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 21:14:44 ; Search time 227.819 Seconds
(without alignments)
15856.428 Million cell updates/sec

Title: US-08-908-884-2

Perfect score: 2104

Sequence: 1 TCGAUTCCTTAAACCAATCCA.....ATAAAAAATAAAAA 2104

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	2104	100.0	2104	19 AAV16851	Arabidopsis thalia
2	2009.4	95.5	2011	19 AAV46274	A. thaliana NIM-1
3	2006.2	95.4	2011	19 AAV46275	A. thaliana NIM-1
4	2006.2	95.4	2011	19 AAV43661	Non-inducible immu
5	1993.6	94.8	2024	21 AAC37765	Arabidopsis thalia
6	1760	83.7	5655	19 AAV46273	A. thaliana NIM-1
7	1760	83.7	5655	19 AAV43659	A. thaliana non-in
8	1760	83.7	5655	19 AAV04632	Arabidopsis thalia
9	1760	83.7	9919	19 AAV43658	A. thaliana non-in

C	10	1760	83.7	9919	19 AAV04631	Arabidopsis thalia
	11	1748.4	83.1	7548	19 AAV16850	Arabidopsis thalia
	12	1605	76.3	1608	19 AAV46277	A. thaliana C-term
	13	1605	76.3	1608	19 AAV43663	Non-inducible immu
	14	1592.8	75.7	1597	19 AAV46276	A. thaliana N-term
	15	1592.8	75.7	1597	19 AAV43662	Non-inducible immu
	16	1188.4	56.5	1194	19 AAV46278	A. thaliana C- and
	17	1188.4	56.5	1194	19 AAV43664	Non-inducible immu
	18	980.4	46.6	1740	21 AAV97192	B. napus NIM1 homo
	19	951.8	45.2	1803	21 AAV97202	A. thaliana NIM1 h
	20	951.8	45.2	1818	21 AAV97233	A. thaliana NIM1 h
	21	781.4	37.1	786	19 AAV46279	A. thaliana NIM-1
	22	781.4	37.1	786	19 AAV43665	Non-inducible immu
	23	579	27.5	1731	21 AAV97191	L. esculentum NIM1
	24	578.4	27.5	1767	21 AAV97190	N. tabacum NIM1 ho
	25	578.4	27.5	2172	19 AAV16852	Nicotiana glutinos
	26	554	26.3	2299	21 AAV97229	B. vulgaris NIM1 h
	27	422.2	20.1	2040	22 AAC8457	Rice putative nega
	28	419	19.9	2194	21 AAA61047	cDNA sequence enco
	29	360.4	17.1	1565	22 AAH43382	cDNA sequence enco
	30	314.6	15.0	1668	22 AAH43384	cDNA sequence enco
	31	290.8	13.8	653	21 AAV97219	S. tuberosum NIM1
	32	288	13.7	659	21 AAV97211	N. tabacum NIM1 ho
	33	284.2	13.5	498	21 AAV97225	B. napus NIM1 homo
	34	263.6	12.5	2673	21 AAC97234	N. tabacum NIM1 ho
	35	260.2	12.4	2368	22 AAC84340	Rice Nph1 cDNA seq
	36	258.6	12.3	1428	22 AAC84339	Rice Nph1 protein
	37	258.6	12.3	2326	22 AAH43381	cDNA sequence enco
	38	256.2	12.2	2069	21 AAA61048	Rice putative nega
	39	241.6	11.5	4270	22 AAH43377	DNA sequence enco
	40	233	11.1	498	21 AAV97215	L. esculentum NIM1
	41	232.6	11.1	2154	21 AAC68800	Maize NPRI coding
	42	228.6	10.9	1761	21 AAV97193	A. thaliana NIM1 h
	43	228.4	10.9	2171	21 AAC46995	Arabidopsis thalia
	44	228.2	10.8	498	21 AAV97216	B. vulgaris NIM1 h
	45	225	10.7	2844	21 AAA97230	H. annuus NIM1 homo

ALIGNMENTS

RESULT 1

AAV16851

ID AAV16851 standard; cDNA; 2104 BP.

XX AAV16851;

AC AAV16851;

DT 17-AUG-1998 (first entry)

DE Arabidopsis thaliana acquired resistance gene NPRI.

XX NPRI gene; acquired resistance; disease; plant pathogens; bacteria;

KW mycoplasma; fungi; insects; nematodes; viruses; viroids;

KW transgenic; ds.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 93..1874

FT /*tag- a

FT /product- acquired resistance protein

FT /note= NPRI gene

PN WO9806748-A1.

PD 19-FEB-1998.

PF 08-AUG-1997; 97WO-US13994.

PR 16-MAY-1997; 97US-0046769.

PR 09-AUG-1996; 96US-0023851.

PR 10-JAN-1997; 97US-0035166.


```
Db 1741 AGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAATTCGTCCTCGACAG 1800
QY 1801 ATTCGACTTCTCCACATCGAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTC 1860
Db 1801 ATTCGACTTCTCCACATCGAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTC 1860
QY 1861 ATCGTGGTGGTGAGACTCTTCCCTCTTAGTGTAAATTTTGTGTGTFACCATATAATTCGT 1920
Db 1861 ATCGTGGTGGTGAGACTCTTCCCTCTTAGTGTAAATTTTGTGTGTFACCATATAATTCGT 1920
QY 1921 TTTCATGATGACTGTAAGTCTTATGCTATGCTGCGGTGCATATAGTTTCGCTCTTCGT 1980
Db 1921 TTTCATGATGACTGTAAGTCTTATGCTATGCTGCGGTGCATATAGTTTCGCTCTTCGT 1980
QY 1981 TTTCATGATGACTGTAAGTCTTATGCTATGCTGCGGTGCATATAGTTTCGCTCTTCGT 2040
Db 1981 TTTCATGATGACTGTAAGTCTTATGCTATGCTGCGGTGCATATAGTTTCGCTCTTCGT 2040
QY 2041 CCAATGGTATACAGATTTGTAATATATATTTATGTFACATCAACATAAAAAA 2100
Db 2041 CCAATGGTATACAGATTTGTAATATATATTTATGTFACATCAACATAAAAAA 2100
QY 2101 AAAA 2104
Db 2101 AAAA 2104

RESULT 2
AAV46274
ID AAV46274 standard; cdna; 2011 BP.
XX
AC AAV46274;
XX
DT 16-OCT-1998 (first entry)
DE
DE A. thaliana NIM-1 CDNA.
XX
KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 43..1824
FT /*tag= a
FT /product= NIM-1
XX
XX WO9829537-A2.
XX
XX 09-JUL-1998.
XX
XX 23-DEC-1997; 97WO-EP07253.
XX
XX 10-JAN-1997; 97US-0035024.
XX
XX 27-DEC-1996; 96US-0034378.
XX
XX (NOVS ) NOVARTIS AG.
XX
XX
XX Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;
XX WPI; 1998-388119/33.
XX P-PSDB; AAW64435.
XX
XX Protection of immunomodulated plants against pathogens - comprises
XX applying microbicide to provide increase in resistance
XX
XX Disclosure; Page 112-115; 164pp; English.
XX
XX This cDNA sequence encodes the NIM-1 protein from Arabidopsis thaliana.
XX This protein is used in a method resulting in the protection of an
XX immunomodulated plant having a first level of resistance and involves
XX treatment with at least 1 microbicide that confers a second level of
```

```
CC resistance, such that the plants have a third level of resistance greater
CC than the sum of the first two levels. The method can be applied to a wide
CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
CC against viruses, fungi, bacteria, insects and nematodes. The method
CC provides a high level of resistance and allows a reduction in the amount
CC of microbicide used. Since the process involves two different methods of
CC protection, it is unlikely that the pathogen will develop resistance to
CC the treatment.
XX
SQ Sequence 2011 BP; 563 A; 417 C; 472 G; 559 T; 0 other;
Query Match 95.5%; Score 2009.4; DB 19; Length 2011;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 51 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCACATTGAT 110
Db 1 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCACATTGAT 60
QY 111 GGATTCGCCGATTTCTATGAATCAGACGACATAGTTTCGTCGCTACCGAATAACACCGAC 170
Db 61 GGATTCGCCGATTTCTATGAATCAGACGACATAGTTTCGTCGCTACCGAATAACACCGAC 120
QY 171 TCCTCTATTCTTTATCTGCGCGCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 230
Db 121 TCCTCTATTGTTATCTGCGCGCGAACAAGTACTCACCGGACCTGATGTATCTGCTCTG 180
QY 231 CAATTGCTCTCCAACAGCTTCGAATCCGCTTTTGACTCGCGCGGATGATTTCTACACGGAC 290
Db 181 CAATTGCTCTCCAACAGCTTCGAATCCGCTTTTGACTCGCGCGGATGATTTCTACACGGAC 240
QY 291 GCTAAGCTTGTCTCTCCGACGCGCGGGAAGTTTCTTCCACCGGTGCGTTTGTGTCAGCG 350
Db 241 GCTAAGCTTGTCTCTCCGACGCGCGGGAAGTTTCTTCCACCGGTGCGTTTGTGTCAGCG 300
QY 351 AGAAGCTCTTTCTCAAGAGCGCTTTTAGCGCGCGCTTAAGAAGAGAGAACTCCAACAAC 410
Db 301 AGAAGCTCTTTCTCAAGAGCGCTTTTAGCGCGCGCTTAAGAAGAGAGAACTCCAACAAC 360
QY 411 ACCGCGCGCGTGAACTCGAGCTTAAGAGATTTGCAAGGATTTACGAAGTCGCTTTTCGAT 470
Db 361 ACCGCGCGCGTGAACTCGAGCTTAAGAGATTTGCAAGGATTTACGAAGTCGCTTTTCGAT 420
QY 471 TCGGTTGTGACTGTTTGTGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAGA 530
Db 421 TCGGTTGTGACTGTTTGTGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAGA 480
QY 531 GTTCTGTAATGCGCAGCAGAGAAATTTGCTGCCACGCTGGCTTGGCGCGCGCGGTGGATTTC 590
Db 481 GTTCTGTAATGCGCAGCAGAGAAATTTGCTGCCACGCTGGCTTGGCGCGCGCGGTGGATTTC 540
QY 591 ATGTTGGAGGTTCTCTATTGCTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTAT 650
Db 541 ATGTTGGAGGTTCTCTATTGCTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTAT 600
QY 651 CAGAGCAGCTTATTTGACGCTTCTAGACAAAGTTGTATAGAGACACATTTGTTTACTCTC 710
Db 601 CAGAGCAGCTTATTTGACGCTTCTAGACAAAGTTGTATAGAGACACATTTGTTTACTCTC 660
QY 711 AAGCTTGTCTAATATATGTTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT 770
Db 661 AAGCTTGTCTAATATATGTTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT 720
QY 771 ATGTGCAAGTCTAATGATAGATGTTAGTCTTTGAAAAGTCAATCCCGGAAGAGCTTCTT 830
Db 721 ATGTGCAAGTCTAATGATAGATGTTAGTCTTTGAAAAGTCAATCCCGGAAGAGCTTCTT 780
QY 831 AAAGAGATAATTGATAGAGCTAAAGAGCTTGTGTTGGAGGTACCTAAAGTAAGAAACAT 890
Db 781 AAAGAGATAATTGATAGAGCTAAAGAGCTTGTGTTGGAGGTACCTAAAGTAAGAAACAT 840
QY 891 GTCTCGAATGTACATAAGGCAGCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950
Db 841 GTCTCGAATGTACATAAGGCAGCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG
```


Db 841 GTCTCGAATGTACATAAAGGCACCTTGACTCGCATGATATTGAGTTAGTCAAGTTGCTTTTG 900
QY 951 AAAGAGGATCACACCAATCTAGATGCGTGTCTCTCTCAATTCGCTGTTGCAATATGC 1010
Db 901 AAAGAGGATCACACCAATCTAGATGCGTGTCTCTCTCAATTCGCTGTTGCAATATGC 960
QY 1011 AATGTGAGAGCGGCAACAGATCTTTTAAACTTGATCTTGCCGATGTCACCAATAGGAAT 1070
Db 961 AATGTGAGAGCGGCAACAGATCTTTTAAACTTGATCTTGCCGATGTCACCAATAGGAAT 1020
QY 1071 CCGAGGGATATACGGTCTCTCATCTTCTGCGATGCGGAAGAGGCCACCAATTTGATACTA 1130
Db 1021 CCGAGGGATATACGGTCTCTCATCTTCTGCGATGCGGAAGAGGCCACCAATTTGATACTA 1080
QY 1131 TCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC 1190
Db 1081 TCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC 1140
QY 1191 ATGATCGCAAAACAGCCACTATGCGCTTGAATGTAATAATATCCCGAGCAATGCAAG 1250
Db 1141 ATGATCGCAAAACAGCCACTATGCGGTTGAATGTAATAATATCCCGAGCAATGCAAG 1200
QY 1251 CATTTCTCTCAAAAGCGGCACTATGTGTAGAAATTAAGAGCAAGAGCAACACGAGAACAA 1310
Db 1201 CATTTCTCTCAAAAGCGGCACTATGTGTAGAAATTAAGAGCAAGAGCAACACGAGAACAA 1260
QY 1311 ATTCTCTAGAGATGTTCTCTCCCTCTTTTGCAGTGGCGGCGGATGAATTTGAAATGACGCTG 1370
Db 1261 ATTCTCTAGAGATGTTCTCTCCCTCTTTTGCAGTGGCGGCGGATGAATTTGAAATGACGCTG 1320
QY 1371 CTCGATCTTGAATAAGAGTTGCACCTTGCTCAACGCTCTTTTCCAAAGCAAGCAAGCT 1430
Db 1321 CTCGATCTTGAATAAGAGTTGCACCTTGCTCAACGCTCTTTTCCAAAGCAAGCAAGCT 1380
QY 1431 GCAATGGAGATCGCCGAAATGAAGGAAACATGTAGTTATAGTCACTAGCCTCGAGCCT 1490
Db 1381 GCAATGGAGATCGCCGAAATGAAGGAAACATGTAGTTATAGTCACTAGCCTCGAGCCT 1440
QY 1491 GACCGTCTCAGTGTACGAGAGACATCACCGGTGTAAAGATAGCACCTTTTCAGAAATC 1550
Db 1441 GACCGTCTCAGTGTACGAGAGACATCACCGGTGTAAAGATAGCACCTTTTCAGAAATC 1500
QY 1551 CTAGAAGAGCATCAAGTAGACTAAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGA 1610
Db 1501 CTAGAAGAGCATCAAGTAGACTAAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGA 1560
QY 1611 TTCTTCCCGCGCTGTTCCGCGAGTCTCGACAGATATGAACCTTGAGGACTTGACTCAA 1670
Db 1561 TTCTTCCCGCGCTGTTCCGCGAGTCTCGACAGATATGAACCTTGAGGACTTGACTCAA 1620
QY 1671 CTGGCTTGGGAGAACGACACTGCTGAGAAACGACTACAAAAGCAAGGTACATG 1730
Db 1621 CTGGCTTGGGAGAACGACACTGCTGAGAAACGACTACAAAAGCAAGGTACATG 1680
QY 1731 GAAATCAAGAGACACTAAGAAAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAATTCG 1790
Db 1681 GAAATCAAGAGACACTAAGAAAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAATTCG 1740
QY 1791 TCCTCGACAGATTCGACTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGT 1850
Db 1741 TCCTCGACAGATTCGACTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGT 1800
QY 1851 AAACCTCTCATGCTCGTGGTGAGACTCTTGCCCTTTAGTGTAAATTTTGTGTACCAT 1910
Db 1801 AAACCTCTCATGCTCGTGGTGAGACTCTTGCCCTTTAGTGTAAATTTTGTGTACCAT 1860
QY 1911 ATAATCTGTTTTCATGATGACTGTAACTGTTTATCTCTATCTGTCGCTCATATAGTTT 1970
Db 1861 ATAATCTGTTTTCATGATGACTGTAACTGTTTATCTCTATCTGTCGCTCATATAGTTT 1920
QY 1971 CGCTCTTCGTTTTCGATCTCTGTATTAATTCGTGCAAGGTGTGCTTCAAAACAAATGTTGA 2030
Db 1921 CGCTCTTCGTTTTCGATCTCTGTATTAATTCGTGCAAGGTGTGCTTCAAAACAAATGTTGA 1980

QY 2031 ACAATTTGACCAATGGTATACAGATTGTA 2061
Db 1981 ACAATTTGACCAATGGTATACAGATTGTA 2011

RESULT 3

AAV46275
ID AAV46275 standard; cDNA; 2011 BP.

XX AAV46275;

XX AC

XX 16-OCT-1998 (first entry)

XX A. thaliana NIM-1 cDNA variant #1.

XX NIM-1; noninducible immunity; systemic acquired resistance; SAR;

KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;

KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.

XX Arabidopsis thaliana.

OS Synthetic.

XX key Location/Qualifiers

XX CDS 43..1824

XX FT /*tag= a

XX FT /product= NIM-1

XX FT /note= "variant"

XX FT mutation 205..207

XX FT /*tag= b

XX FT /note= "wild type TCC is replaced by GCC"

XX FT mutation 217..219

XX FT /*tag= c

XX FT /note= "wild type TCG is replaced by GCG"

XX WO9829537-A2.

XX 09-JUL-1998.

XX 23-DEC-1997; 97WO-EP07253.

XX 10-JAN-1997; 97US-0035024.

XX 27-DEC-1996; 96US-0034378.

XX (NOVS) NOVARTIS AG.

XX Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;

XX WPT; 1998-388119/33.

XX P-PSDB; AAW64436.

XX Protection of immunomodulated plants against pathogens - comprises

XX applying microbicide to provide increase in resistance

XX Claim 11; Page 116-120; 164pp; English.

XX This sequence encodes a variant NIM-1 protein from Arabidopsis

CC thaliana. This protein is used in a method resulting in the protection of

CC an immunomodulated plant having a first level of resistance and involves

CC treatment with at least 1 microbicide that confers a second level of

CC resistance, such that the plants have a third level of resistance greater

CC than the sum of the first two levels. The method can be applied to a wide

CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect

CC against viruses, fungi, bacteria, insects and nematodes. The method

CC provides a high level of resistance and allows a reduction in the amount

CC of microbicide used. Since the process involves two different methods of

CC protection, it is unlikely that the pathogen will develop resistance to

CC the treatment.

XX Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;

Query Match 95.4%; Score 2006.2; DB 19; Length 2011;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 2008: Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
QY	51	GATCTCTTTAAATTTGTAATTTCAATTCATCGGAACCTGTTGATGGACACACCACCATTTGAT	110
Db	1	GATCTCTTTAAATTTGTAATTTCAATTCATCGGAACCTGTTGATGGACACACCACCATTTGAT	60
QY	111	GGATTCCGCGATTCTTATSAATATCAGCAGCACTAGTTTCGTCGATACCGATPAACACCCAC	170
Db	61	GGATTCCGCGATTCTTATSAATATCAGCAGCACTAGTTTCGTCGATACCGATPAACACCCAC	120
QY	171	TCCTCTATTGTTTATCTGCGCGCCGAACAAGTACTCAGCGACCTGATGTATCTGCTCTG	230
Db	121	TCCTCTATTGTTTATCTGCGCGCCGAACAAGTACTCAGCGACCTGATGTATCTGCTCTG	180
QY	231	CAATTGCTCTCCAACAGCTTCGAATCCGTCCTTTGACTCGCGGATGATTTCTACAGGAC	290
Db	181	CAATTGCTCTCCAACAGCTTCGAAGCCGTCCTTTGACGCGCGGATGATTTCTACAGGAC	240
QY	291	GCTAAGCTTGTCTCTCCAGCGCGGGAAGTTCTTTCCACCGTGGGTTTGTCTACGG	350
Db	241	GCTAAGCTTGTCTCTCCAGCGCGGGAAGTTCTTTCCACCGTGGGTTTGTCTACGG	300
QY	351	AGAAGCTCTTCTTCAAGAGCGCTTTAGCGCGCTAAGAAGGAGAAAGACTCCCAACAAC	410
Db	301	AGAAGCTCTTCTTCAAGAGCGCTTTAGCGCGCTAAGAAGGAGAAAGACTCCCAACAAC	360
QY	411	ACCGCGCGGTGAAGCTCAGCTTAAGGAGATTGCAAGGATTACGAAGTCGGTTTCGAT	470
Db	361	ACCGCGCGGTGAAGCTCAGCTTAAGGAGATTGCAAGGATTACGAAGTCGGTTTCGAT	420
QY	471	TCGGTTGTGACTCTTTTGGCTTATGTTTACAGCAGCAGTGAGACCGCCGCTTAAGGA	530
Db	421	TCGGTTGTGACTCTTTTGGCTTATGTTTACAGCAGCAGTGAGACCGCCGCTTAAGGA	480
QY	531	GTTTCTGAATGCGCAGCAGAGAAATGCTGCCACGTGGTTCGCCGCGCGGTGGATTC	590
Db	481	GTTTCTGAATGCGCAGCAGAGAAATGCTGCCACGTGGTTCGCCGCGCGGTGGATTC	540
QY	591	ATGCTGGAGGTCTCTATTTGGCTTTCATCTCAAGATCCCTGAATTAATTACTCTCAT	650
Db	541	ATGCTGGAGGTCTCTATTTGGCTTTCATCTCAAGATCCCTGAATTAATTACTCTCAT	600
QY	651	CAGAGGCACCTATTGGACGCTTGAGACAAAGTTGTTATAGAGACACATTTGGTTATATCT	710
Db	601	CAGAGGCACCTATTGGACGCTTGAGACAAAGTTGTTATAGAGACACATTTGGTTATATCT	660
QY	711	AAGCTTGTCTAATATATGTTGAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT	770
Db	661	AAGCTTGTCTAATATATGTTGAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT	720
QY	771	ATTGTCAAGTCTAATCTAGATATGGTTAGTCTTGAAGTCAATGCCGGAAGAGCTTGT	830
Db	721	ATTGTCAAGTCTAATCTAGATATGGTTAGTCTTGAAGTCAATGCCGGAAGAGCTTGT	780
QY	831	AAAGAGATAATGATAGACGTAAGAGCTTGGTTGGAGGTACCTAAAGTAAGAAACAT	890
Db	781	AAAGAGATAATGATAGACGTAAGAGCTTGGTTGGAGGTACCTAAAGTAAGAAACAT	840
QY	891	GTCTCGAATCTACATAAGGCATTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG	950
Db	841	GTCTCGAATCTACATAAGGCATTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG	900
QY	951	AAAGAGGATCACCAATCTAGATGATGCGTGTCTTTCATTTTCGCTGTTGCAATATTC	1010
Db	901	AAAGAGGATCACCAATCTAGATGATGCGTGTCTTTCATTTTCGCTGTTGCAATATTC	960
QY	1011	AATGTGAAGCCGCAACAGATCTTTTAAACTTGATCTTGGCGATGTCACCAATAGGAAT	1070
Db	961	AATGTGAAGCCGCAACAGATCTTTTAAACTTGATCTTGGCGATGTCACCAATAGGAAT	1020
QY	1071	CCGAGGGGATATACGTTGCTTCTCATGTTGCTGCGGAGGAGCCCAATTTGATACTA	1130
Db	1021	CCGAGGGGATATACGTTGCTTCTCATGTTGCTGCGGAGGAGCCCAATTTGATACTA	1080

QY	1131	TCCTCTATTGGAAGAGTGCAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC	1190
Db	1081	TCCTCTATTGGAAGAGTGCAGTGCATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC	1140
QY	1191	ATGATCGGAAAACAAGCCACTATGGCGTTTGAATGTAAATATATCCGGAGCAATGCAAG	1250
Db	1141	ATGATCGGAAAACAAGCCACTATGGCGTTTGAATGTAAATATATCCGGAGCAATGCAAG	1200
QY	1251	CATTCTCTCAAGAGCGGACTATGTGTAGAAATACTAGAGCAAGAGACAAACGAGAAACA	1310
Db	1201	CATTCTCTCAAGAGCGGACTATGTGTAGAAATACTAGAGCAAGAGACAAACGAGAAACA	1260
QY	1311	ATTCTCTAGAGATGTTCCCTCCCTCTTTTGCAGTGGCGCGGATGAATTAAGATGACCGCT	1370
Db	1261	ATTCTCTAGAGATGTTCCCTCCCTCTTTTGCAGTGGCGCGGATGAATTAAGATGACCGCT	1320
QY	1371	CTCGATCTTGAANAATAGAGTTGCACCTTCTCAACGCTCTTTTCCAAACGAGACAAAGCT	1430
Db	1321	CTCGATCTTGAANAATAGAGTTGCACCTTCTCAACGCTCTTTTCCAAACGAGACAAAGCT	1380
QY	1431	GCAATGGAGATCGCGAAATGAAGGAAACATGTGAGTTTCATAGTACTGACCTCGAGCCT	1490
Db	1381	GCAATGGAGATCGCGAAATGAAGGAAACATGTGAGTTTCATAGTACTGACCTCGAGCCT	1440
QY	1491	GACCTCTCACTGGTACGAGAGAACATCCCGGCTGTAAAGATAGCACCTTCAGAAATC	1550
Db	1441	GACCTCTCACTGGTACGAGAGAACATCCCGGCTGTAAAGATAGCACCTTCAGAAATC	1500
QY	1551	CTAGAAGAGCATCAAAAGTAGACTAAAAGCGCTTCTTAAACCGCTGGAACCTCGGAAACGA	1610
Db	1501	CTAGAAGAGCATCAAAAGTAGACTAAAAGCGCTTCTTAAACCGCTGGAACCTCGGAAACGA	1560
QY	1611	TTCTTCCCGCGCTGTTCCGCACTGCTCGACAGATTATGAACCTGTGAGGACTTGACTCAA	1670
Db	1561	TTCTTCCCGCGCTGTTCCGCACTGCTCGACAGATTATGAACCTGTGAGGACTTGACTCAA	1620
QY	1671	CTGGCTTTCGGGAGAACGACACTGCTGAGAAACGACTACAAAAGCAAGGTACATG	1730
Db	1621	CTGGCTTTCGGGAGAACGACACTGCTGAGAAACGACTACAAAAGCAAGGTACATG	1680
QY	1731	GAATAACAAGAGACACTAAAGAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCG	1790
Db	1681	GAATAACAAGAGACACTAAAGAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCG	1740
QY	1791	TCCTCAGCAGATTCGACTTCTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGT	1850
Db	1741	TCCTCAGCAGATTCGACTTCTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGT	1800
QY	1851	AAACTCTCATCGTGGTGGAGACTCTTCCCTCTTAGTGTAATTTTCTGTGACCAT	1910
Db	1801	AAACTCTCATCGTGGTGGAGACTCTTCCCTCTTAGTGTAATTTTCTGTGACCAT	1860
QY	1911	ATAATTTCTGTTTCATGATGACTGTAACCTGTTATGCTATCGTTGGCGCTCATATAGTTT	1970
Db	1861	ATAATTTCTGTTTCATGATGACTGTAACCTGTTATGCTATCGTTGGCGCTCATATAGTTT	1920
QY	1971	CGCTCTCGTTTTCGATCCTCTGTATTTATTTGCTGAGGTGTGCTTCAACAAATGTTGTA	2030
Db	1921	CGCTCTCGTTTTCGATCCTCTGTATTTATTTGCTGAGGTGTGCTTCAACAAATGTTGTA	1980
QY	2031	ACAATTTGAACCAATGGTATACAGATTTGTA	2061
Db	1981	ACAATTTGAACCAATGGTATACAGATTTGTA	2011

RESULT 4
AAV43661
ID AAV43661 standard; cDNA; 2011 BP.
XX
XX AAV43661;
XX
DT 29-SEP-1998 (first entry)

XX DE Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA.
XX KW Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;
XX KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;
XX KW constitutive immunity; agriculture; variant; ss.
XX OS Arabidopsis thaliana.
XX OS Synthetic.
XX PH Location/Qualifiers
XX FT 43..1824
XX FT CDS
XX FT /*tag= a "NIM1 protein variant 1"
XX FT /product= "NIM1 protein variant 1"
XX FT 205..207
XX FT mutation
XX FT /*tag= b
XX FT /note= "wild type TGC is replaced by GCC"
XX FT 217..219
XX FT mutation
XX FT /*tag= c
XX FT /note= "wild type TGC is replaced by GCG"
XX PN W09826082-Al.
XX PD 18-JUN-1998.
XX XX
XX PF 12-DEC-1997; 97WO-EP07012.
XX PR 20-JUN-1997; 97US-0880179.
XX PR 13-DEC-1996; 96US-0033177.
XX PR 27-DEC-1996; 96US-0034379.
XX PR 27-DEC-1996; 96US-0034382.
XX PR 10-JAN-1997; 97US-0034730.
XX PR 10-JAN-1997; 97US-0035021.
XX PR 10-JAN-1997; 97US-0035022.
XX PA (NOVS) NOVARTIS AG.
XX PI Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;
XX PI Uknes SJ;
XX XX
XX DR WPI: 1998-348536/30.
XX DR P-PSDB; AAW61983.
XX PT Use of non-inducible immunity-1 gene - for transforming plants to
XX PT produce transgenic plants having a broad spectrum disease resistance
XX PS Claim 5; Pages 140-144; 205pp; English.
XX CC This cDNA encodes an altered form of the Arabidopsis thaliana non-
XX CC inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
XX CC AAV43665 represent variants of the NIM1 cDNA. The invention provides a
XX CC chimeric gene comprising a promoter active in plants operatively linked
XX CC to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
XX CC cells stably transformed with a recombinant vector comprising such a
XX CC chimeric gene have a broad spectrum of disease resistance. The altered
XX CC NIM1 proteins act as dominant-negative regulators of the systemic
XX CC acquired resistance (SAR) signal transduction pathway. The transgenic
XX CC plants transformed with an altered NIM1 gene exhibits constitutive SAR
XX CC expression which is higher in the transformed plants than in a wild-type
XX CC plant. The products can be used for producing plants with a broad
XX CC spectrum disease resistance. Overexpression of NIM1 mimics the effects
XX CC of inducer compounds that induce constitutive immunity (CIM) phenotype
XX CC in plants. The inventions can be used with plants such as rice, wheat,
XX CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
XX CC chichory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
XX CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
XX CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
XX CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
XX CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
XX CC tomato, sorghum and sugarcane. The plants produced are resistant to
XX CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such
XX CC as aphids and lepidoptera and nematodes. The plants produced can be used
XX CC in agriculture.

XX SQ Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;
Query Match 95.4%; Score 2006.2; DB 19; Length 2011;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2008; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 51 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGACACCAACCATTTGAT 110
DB 1 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGACACCAACCATTTGAT 60
QY 111 GGATTCGCCGATTTCTTATGAAATTCAGCAGCACTAGTTTCGTCGCTACCGATTAACACCGAC 170
DB 61 GGATTCGCCGATTTCTTATGAAATTCAGCAGCACTAGTTTCGTCGCTACCGATTAACACCGAC 120
QY 171 TCCTCTATGTTTATCTGCGCGCGGAACAGTACTCACCGGACCTGATGTATCTGCTCTG 230
DB 121 TCCTCTATGTTTATCTGCGCGCGGAACAGTACTCACCGGACCTGATGTATCTGCTCTG 180
QY 231 CAATTCGCTCTCCCAACAGCTTCGGAATCCGTCCTTTGACTCGCCGGATGATTTCTACAGCGAC 290
DB 181 CAATTCGCTCTCCCAACAGCTTCGGAAGCGCTTTGACGCGCGGATGATTTCTACAGCGAC 240
QY 291 GCTAAGCTTGTCTCTCCGACGCGCGGAAGTTTCTTTCCACCGGTGCGTTTGTTCAGCG 350
DB 241 GCTAAGCTTGTCTCTCCGACGCGCGGAAGTTTCTTTCCACCGGTGCGTTTGTTCAGCG 300
QY 351 AGAAGCTCTTTCTTCAAGAGCGCTTTAGCGCGCTTAAAGAGGAGAAAGACTCCAACAAC 410
DB 301 AGAAGCTCTTTCTTCAAGAGCGCTTTAGCGCGCTTAAAGAGGAGAAAGACTCCAACAAC 360
QY 411 ACCGCCCGCGTGAAGCTCGAGCTTAAAGAGATTGCCAAGGATTACGAAGTTCGGTTTCGAT 470
DB 361 ACCGCCCGCGTGAAGCTCGAGCTTAAAGAGATTGCCAAGGATTACGAAGTTCGGTTTCGAT 420
QY 471 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGGA 530
DB 421 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGGA 480
QY 531 GTTTCTGAATCGCAGACGAGAAATGCTGCGACGTGGCTTCCCGCGCGCGGTGGATTTTC 590
DB 481 GTTTCTGAATCGCAGACGAGAAATGCTGCGACGTGGCTTCCCGCGCGCGGTGGATTTTC 540
QY 591 ATGTTGGAGGTTCTCTATTTGGCTTCTTCAAGATCCCTGAATTAATTAATTAATTAAT 650
DB 541 ATGTTGGAGGTTCTCTATTTGGCTTCTTCAAGATCCCTGAATTAATTAATTAATTAAT 600
QY 651 CAGAGGCACCTATTGGACGTTGTAGACAAAGTTGTTATAGAGACACATTTGGTTATACTC 710
DB 601 CAGAGGCACCTATTGGACGTTGTAGACAAAGTTGTTATAGAGACACATTTGGTTATACTC 660
QY 711 AAGCTTGTCTAATATATGTTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTTAAAGAGATT 770
DB 661 AAGCTTGTCTAATATATGTTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTTAAAGAGATT 720
QY 771 ATGTCGAAGCTAATATAGATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 830
DB 721 ATGTCGAAGCTAATATAGATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 780
QY 831 AAAGAGATAATTGATAGACGTTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT 890
DB 781 AAAGAGATAATTGATAGACGTTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAGAAACAT 840
QY 891 GTCCTGAATGTACATAAGGCACTTACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTTC 950
DB 841 GTCCTGAATGTACATAAGGCACTTACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTTC 900
QY 951 AAAGAGGATCACCAATCTAGATGATGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1010
DB 901 AAAGAGGATCACCAATCTAGATGATGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
QY 1011 AATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCCGATGTCAACCACTAGGAAT 1070
DB 960 AATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCCGATGTCAACCACTAGGAAT 1020

Db	961	AATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTGCCGATGCAACCATAGCAAT	1020	ID	AAC37765 standard; DNA; 2024 BP.
Qy	1071	CCGAGGGATATACGGTGCTTCATGTGCTCGCATGCGGAGGAGCCACAAATTCATACTA	1130	XX	
Db	1021	CCGAGGGATATACGGTGCTTCATGTGCTCGCATGCGGAGGAGCCACAAATTCATACTA	1080	AC	AAC37765;
Qy	1131	TCTCTATTGGAAGAGGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC	1190	XX	17-OCT-2000 (first entry)
Db	1081	TCTCTATTGGAAGAGGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC	1140	DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 18587.
Qy	1191	ATGATCGCAAAACAGCACTATGCGGGTGAATGTATATATATCCCGGAGCAATGCAAG	1250	XX	Hybridisation assay; genetic mapping; gene expression control;
Db	1141	ATGATCGCAAAACAGCACTATGCGGGTGAATGTATATATATCCCGGAGCAATGCAAG	1200	KW	protein identification; signal transduction pathway;
Qy	1251	CATTCTCTCAAGGCCGACTATGTGTAGAAATACTACAGCAAGAGACAACAGAGACAA	1310	KW	metabolic pathway; promoter; termination sequence; ss.
Db	1201	CATTCTCTCAAGGCCGACTATGTGTAGAAATACTACAGCAAGAGACAACAGAGACAA	1260	XX	Arabidopsis thaliana.
Qy	1311	ATTCTTAGAGATGTCTCCTCCTCTTTTGCAGTGGCGCCGATGAATTTGAAGATGACGCTG	1370	XX	EP1033405-A2.
Db	1261	ATTCTTAGAGATGTCTCCTCCTCTTTTGCAGTGGCGCCGATGAATTTGAAGATGACGCTG	1320	PD	06-SEP-2000.
Qy	1371	CTCGATCTTGAANAATAGAGTTGCACTTGCTCAAGCTCTTTTCCACGGAAGCACAAAGCT	1430	XX	25-FEB-2000; 2000EP-0301439.
Db	1321	CTCGATCTTGAANAATAGAGTTGCACTTGCTCAAGCTCTTTTCCACGGAAGCACAAAGCT	1380	PR	25-FEB-1999; 99US-0121825.
Qy	1431	GCAATGGAGATCGCGAAATGAAGGGAACATGTGAGTTCATAGTACTAGCCTCGAGCCT	1490	PR	05-MAR-1999; 99US-0123180.
Db	1381	GCAATGGAGATCGCGAAATGAAGGGAACATGTGAGTTCATAGTACTAGCCTCGAGCCT	1440	PR	09-MAR-1999; 99US-0123548.
Qy	1491	GACCGTCTACTGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAAATC	1550	PR	23-MAR-1999; 99US-0125788.
Db	1441	GACCGTCTACTGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTCAGAAATC	1500	PR	25-MAR-1999; 99US-0126264.
Qy	1551	CTAGAAGAGATCAAGTAGACTAAAGAGCGTTTCTAAAACGTTGGAATCGGGAAACGA	1610	PR	29-MAR-1999; 99US-0126785.
Db	1501	CTAGAAGAGATCAAGTAGACTAAAGAGCGTTTCTAAAACGTTGGAATCGGGAAACGA	1560	PR	01-APR-1999; 99US-0127462.
Qy	1611	TTCTTCCCGGCTGTTCGGCAGTGCTCGACGAGATTAAGTGTGAGGACTTGACTCAA	1670	PR	06-APR-1999; 99US-0128234.
Db	1561	TTCTTCCCGGCTGTTCGGCAGTGCTCGACGAGATTAAGTGTGAGGACTTGACTCAA	1620	PR	08-APR-1999; 99US-0128714.
Qy	1671	CTGCTTCCGGAGAACGACACTGCTGTGAGAAACGACTACAAAAGCAAGCAAGGTACATG	1730	PR	16-APR-1999; 99US-0129845.
Db	1621	CTGCTTCCGGAGAACGACACTGCTGTGAGAAACGACTACAAAAGCAAGCAAGGTACATG	1680	PR	19-APR-1999; 99US-0130077.
Qy	1731	GAATACAAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAATTCG	1790	PR	21-APR-1999; 99US-0130449.
Db	1681	GAATACAAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAATTCG	1740	PR	23-APR-1999; 99US-0130510.
Qy	1791	TCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCCT	1850	PR	28-APR-1999; 99US-0130891.
Db	1741	TCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCCT	1800	PR	30-APR-1999; 99US-0131449.
Qy	1851	AAACTCTCATCGTCTCGGTGAGACTCTGCGCTTTAGTGTAAATTTTGTGCTGACCAT	1910	PR	30-APR-1999; 99US-0132048.
Db	1801	AAACTCTCATCGTCTCGGTGAGACTCTGCGCTTTAGTGTAAATTTTGTGCTGACCAT	1860	PR	04-MAY-1999; 99US-0132407.
Qy	1911	ATAATTCGTGTTTCATGACTGTAACGTGTTATGTCTATCGTTGCGGTCATATAGTTT	1970	PR	05-MAY-1999; 99US-0132484.
Db	1861	ATAATTCGTGTTTCATGACTGTAACGTGTTATGTCTATCGTTGCGGTCATATAGTTT	1920	PR	06-MAY-1999; 99US-0132485.
Qy	1971	CGCTCTCGTTTTCGATCCCTGTGTATTATTCGTCGAGGTGTGCTTCAACAAATGTTGTA	2030	PR	07-MAY-1999; 99US-0132863.
Db	1921	CGCTCTCGTTTTCGATCCCTGTGTATTATTCGTCGAGGTGTGCTTCAACAAATGTTGTA	1980	PR	11-MAY-1999; 99US-0132863.
Qy	2031	ACAATTTGAACCAATGGTATACAGATTTGTA 2061		PR	14-MAY-1999; 99US-0134256.
Db	1981	ACAATTTGAACCAATGGTATACAGATTTGTA 2011		PR	14-MAY-1999; 99US-0134218.
RESULT	5			PR	14-MAY-1999; 99US-0134219.
AAC37765				PR	14-MAY-1999; 99US-0134221.
				PR	14-MAY-1999; 99US-0134370.
				PR	19-MAY-1999; 99US-0134768.
				PR	19-MAY-1999; 99US-0134941.
				PR	20-MAY-1999; 99US-0135124.
				PR	21-MAY-1999; 99US-0135353.
				PR	24-MAY-1999; 99US-0135629.
				PR	25-MAY-1999; 99US-0136021.
				PR	27-MAY-1999; 99US-0136392.
				PR	28-MAY-1999; 99US-0136782.
				PR	01-JUN-1999; 99US-0137222.
				PR	03-JUN-1999; 99US-0137528.
				PR	04-JUN-1999; 99US-0137502.
				PR	07-JUN-1999; 99US-0137724.
				PR	08-JUN-1999; 99US-0138094.
				PR	10-JUN-1999; 99US-0138540.
				PR	10-JUN-1999; 99US-0138847.
				PR	14-JUN-1999; 99US-0139119.
				PR	16-JUN-1999; 99US-0139452.
				PR	16-JUN-1999; 99US-0139453.
				PR	17-JUN-1999; 99US-0139492.
				PR	18-JUN-1999; 99US-0139454.
				PR	18-JUN-1999; 99US-0139455.
				PR	18-JUN-1999; 99US-0139456.
				PR	18-JUN-1999; 99US-0139457.
				PR	18-JUN-1999; 99US-0139458.
				PR	18-JUN-1999; 99US-0139459.
				PR	18-JUN-1999; 99US-0139460.

PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	24-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	28-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145313.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-01

Db 181 TCCAAAGCTTCGAATCGCTCTTTGACTCGCGGATGATTTCTACAGGACGCTAAGCTT 240
QY 300 GTTCTCTCGAGCGCGGAGTTTCTTTCCACCGGTGCGTTTGTGTCAGCGAGAAGCTCT 359
Db 241 GTTCTCTCGAGCGCGGAGTTTCTTTCCACCGGTGCGTTTGTGTCAGCGAGAAGCTCT 300
QY 360 TTCTTTCAAGAGCGCTTTAGCGCGCGCTTAAGAGGAGAAAGACTCCAAACAACACCGCGGCC 419
Db 301 TTCTTTCAAGAGCGCTTTAGCGCGCGCTTAAGAGGAGAAAGACTCCAAACAACACCGCGGCC 360
QY 420 GTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGTG 479
Db 361 GTGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGTG 420
QY 480 ACTGTTTGGCTTATGTTTACAGACGAGAGTGAGACCGCGCCCTAAAGGAGTTTCTGAA 539
Db 421 ACTGTTTGGCTTATGTTTACAGACGAGAGTGAGCGCGCCCTAAAGGAGTTTCTGAA 480
QY 540 TCGCAGACGAGAAATGCTGCCAGTGGCTTTCGCGCGCGCGGTGGATTTTCATCTTTGGAG 599
Db 481 TCGCGTGAAGAGATTGCTGCCACGTGCGTWTGCCGTCGCCGCGTGGATTTTCATCTTGGAG 540
QY 600 GTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTATCAGAGGCAC 659
Db 541 GTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTATCAGAGGCAC 600
QY 660 TTATTGGACGTTGTAGACAAAGTTGTTATAGAGCACATTTGGTTTACTCAAGCTTGCT 719
Db 601 TTATTGGACGTTGTAGACAAAGTTGTTATAGAGCACATTTGGTTTACTCAAGCTTGCT 660
QY 720 AATATATGCTAAAGCTTGTATGAAGCTATTTGGATAGATGTAAGAGATTAATTGTCAAG 779
Db 661 AATATATGCTAAAGCTTGTATGAAGCTTGTGGATAGATGTAAGAGATTAATTGTCAAG 720
QY 780 TCTAATGTAGATATGGTTAGTCTTGAAGAAGTCATTTGCCGGAAGAGCTTGTAAAGAGATA 839
Db 721 TCTAATGTAGATATGGTTAGTCTTGAAGAAGTCATTTGCCGGAAGAGCTTGTAAAGAGATA 780
QY 840 ATTGATAGACGTTAAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACATGCTCGCAAT 899
Db 781 ATTGATAGACGTTAAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACATGCTCGCAAT 840
QY 900 GTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAGAGGAT 959
Db 841 GTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAGAGGAT 900
QY 960 CACACCAATCTAGATGATGCGTGTGCTCTTCATTTCCGTTGCTGATATTGCAATGTGAAG 1019
Db 901 CACACCAATCTAGATGATGCGTGTGCTCTTCATTTCCGTTGCTGATATTGCAATGTGAAG 960
QY 1020 ACCGCAACAGATCTTTTAAAACTTGTATGCTTCCGATGTCAACCATAGGAATCCGAGGGGA 1079
Db 961 ACCGCAACAGATCTTTTAAAACTTGTATGCTTCCGATGTCAACCATAGGAATCCGAGGGGA 1020
QY 1080 TATAGGTTGCTTCATGTTGCTGCGATGCGGAAGGAGGCCACAAATTGATPACTATCTCTATTG 1139
Db 1021 TATAGGTTGCTTCATGTTGCTGCGATGCGGAAGGAGGCCACAAATTGATPACTATCTCTATTG 1080
QY 1140 GAAAAAGGTGCAAGTGCATCAGAGCAACTTTTGAAGGTAGAAGTGAACCGCACTCATGATCGCA 1199
Db 1081 GAAAAAGGTGCAAGTGCATCAGAGCAACTTTTGAAGGTAGAAGTGAACCGCACTCATGATCGCA 1140
QY 1200 AAACAAGCCACTATGGGGTTTGAATGTAAATAATATCCCGGAGCAATGCAAGCAATTCCTCTC 1259
Db 1141 AAACAAGCCACTATGGGGTTTGAATGTAAATAATATCCCGGAGCAATGCAAGCAATTCCTCTC 1200
QY 1260 AAAGGCCGACTATGTGTAGAANAATCTAGAGCAAGAGACAAACGAGAACAAATTCCTTAGA 1319
Db 1201 AAAGGCCGACTATGTGTAGAANAATCTAGAGCAAGAGACAAACGAGAACAAATTCCTTAGA 1260
QY 1320 GATGTTCTCCCTCTTTTGGAGTGGCGCGGATGAATTTGAAGATGACGCTGCTCGATCTT 1379
Db 1261 GATGTTCTCCCTCTTTTGGAGTGGCGCGGATGAATTTGAAGATGACGCTGCTCGATCTT 1320

QY 1380 GAAATAGAGTTGCCACTTGCTCAACGCTCTTTTCCAAACGGAAGCACAAAGCTGCAATGGAG 1439
Db 1321 GAAATAGAGTTGCCACTTGCTCAACGCTCTTTTCCAAACGGAAGCACAAAGCTGCAATGGAG 1380
QY 1440 ATCGCCGAAATGAAGGAACATGTGAGTTTCATAGTGACTAGCCTCGAGCCTGACCGCTCTC 1499
Db 1381 ATCGCCGAAATGAAGGAACATGTGAGTTTCATAGTGACTAGCCTCGAGCCTGACCGCTCTC 1440
QY 1500 ACTGGTACGAAGAGAACATCATACCGGGTGTAAAGATAGCACCCTTTCAGAAATTCCTAGAAGAG 1559
Db 1441 ACTGGTACGAAGAGAACATCATACCGGGTGTAAAGATAGCACCCTTTCAGAAATTCCTAGAAGAG 1500
QY 1560 CATCAAAGTAGACTAAAGGCGCTTTCTAAACCGTGGAACTCGGGAAGAGTTCCTCCCG 1619
Db 1501 CATCAAAGTAGACTAAAGGCGCTTTCTAAACCGTGGAACTCGGGAAGAGTTCCTCCCG 1560
QY 1620 CGCTGTTCCGCACTGCTCGACAGATTAATGAAGTGTGAGGACTTGAACCTCAACTGGCTTGC 1679
Db 1561 CGCTGTTCCGCACTGCTCGACAGATTAATGAAGTGTGAGGACTTGAACCTCAACTGGCTTGC 1620
QY 1680 GGAGAAAGACACTGCTGTAGAAACGACTACAAAGAAAGAGGTACATGGAAATACAA 1739
Db 1621 GGAGAAAGACACTGCTGTAGAAACGACTACAAAGAAAGAGGTACATGGAAATACAA 1680
QY 1740 GAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCGCTCCGTGACA 1799
Db 1681 GAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCGCTCCGTGACA 1740
QY 1800 GATTGCACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGCTTAACCGTAAACTCTCT 1859
Db 1741 GATTGCACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGCTTAACCGTAAATCTCT 1800
QY 1860 CATCGTCTCGGTGAGACTCTTGCCTCTTAGTGATATTTTCTGTACCATATTAATTCG 1919
Db 1801 CATCGTCTCGGTGAGACTCTTGCCTCTTAGTGATATTTTCTGTACCATATTAATTCG 1860
QY 1920 TTTTCATGATGACTGTAACCTGTTTATGCTATCTGTTGGCGTCATATAGTTTCGCTCTCG 1979
Db 1861 TTTTCATGATGACTGTAACCTGTTTATGCTATCTGTTGGCGTCATATAGTTTCGCTCTCG 1920
QY 1980 TTTTGCATCTCTGTATTTATGCTGCAAGTGTCTTCAACAAATGTTGTAACAATTTGA 2039
Db 1921 TTTTGCATCTCTGTATTTAGTGTGAGTGTGTTTAAACAAACTTCTTAACAATTTGA 1980
QY 2040 ACCAATGGTATACAGATTTGTAATATATATTTATGTACATCAAC 2083
Db 1981 ACCAGCGGTATACAGATTTGTAATATATATTTATGTACATCAAC 2024

RESULT 6
AAV46273
ID AAV46273 standard; DNA; 5655 BP.
XX
AC AAV46273;
XX
DT 16-Oct-1998 (first entry)
XX
DE A. thaliana NIM-1 genomic DNA.
XX
KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
OS Arabidopsis thaliana.
XX
Key Location/Qualifiers
FH 2787..4866
CDS /*tag= a
FT /product= NIM-1
FT 2787..3347
FT /*tag= b
FT /number= 1

FT intron 3348..3426
/*tag= c
/number= 1
FT exon 3427..4162
/*tag= d
FT intron /number= 2
FT FT 4163..4270
/*tag= e
FT FT /number= 2
FT exon 4271..4474
/*tag= f
FT FT /number= 3
FT FT 4475..4585
/*tag= g
FT FT /number= 3
FT FT 4586..4866
/*tag= h
FT FT /number= 4

XX W09829537-A2.

PN 09-JUL-1998.

XX 23-DEC-1997; 97WO-EP07253..

PR 10-JAN-1997; 97US-0035024.

PR 27-DEC-1996; 96US-0034378.

XX (NOVS) NOVARTIS AG.

PA Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;

PI WPI; 1998-388119/33.

XX P-PSDB; AAN64435.

DR Protection of immunomodulated plants against pathogens - comprises
XX applying microbicide to provide increase in resistance

PT Claim 7; Page 96-103; 164pp; English.

PS This genomic DNA sequence encodes the NIM-1 protein from Arabidopsis
XX thaliana. This protein is used in a method resulting in the protection of
CC an immunomodulated plant having a first level of resistance and involves
CC treatment with at least 1 microbicide that confers a second level of
CC resistance, such that the plants have a third level of resistance greater
CC than the sum of the first two levels. The method can be applied to a wide
CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
CC against viruses, fungi, bacteria, insects and nematodes. The method
CC provides a high level of resistance and allows a reduction in the amount
CC of microbicide used. Since the process involves two different methods of
CC protection, it is unlikely that the pathogen will develop resistance to
CC the treatment.

XX Sequence 5655 BP; 1758 A; 1014 C; 1069 G; 1814 T; 0 other;

SQ Query Match 83.7%; Score 1760; DB 19; Length 5655;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;

QY 1 TCAGATCTTTAACCAATCCAGTTGATAAGGTCTCTTCGTTGATTACGAGATCTCTTTA 60
|||||

DB 2695 TCAGATCTTTAACCAATCCAGTTGATAAGGTCTCTTCGTTGATTACGAGATCTCTTTA 2754
|||||

QY 61 ATTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCAACCATTTGATGGATTCGCCG 120
|||||

DB 2755 ATTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCAACCATTTGATGGATTCGCCG 2814
|||||

QY 121 ATTCTTATGAATACAGACACCTAGTTTCGTCGCTACCGNATAACACCGACTCTCTATTGG 180
|||||

DB 2815 ATTCTTATGAATACAGACACCTAGTTTCGTCGCTACCGNATAACACCGACTCTCTATTGG 2874
|||||

QY 181 TTTATCTGGCCGCGACACAGTACTCACCAGCTGATGATCTGCTGCAATTCCTCT 240
|||||

DB 2875 TTTATCTGGCCGCGACAAAGTACTCACCAGACCTGATGATGATCTGCTCTGCAATTGCTCT 2934
|||||

QY 241 CCAACAGCTTCGAATCCGTCCTTTGACTCGCCGAGATGATTTCTACAGGAGCTTAAGCTTG 300
|||||

DB 2935 CCAACAGCTTCGAATCCGTCCTTTGACTCGCCGAGATGATTTCTACAGCGAGCTTAAGCTTG 2994
|||||

QY 301 TTCTCTCCGAGCGCGGGAAGTTTCTTTCCACCGGTGCGTTTGTGTCAGCGAGAGCTCTT 360
|||||

DB 2995 TTCTCTCCGAGCGCGGGAAGTTTCTTTCCACCGGTGCGTTTGTGTCAGCGAGAGCTCTT 3054
|||||

QY 361 TCTTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCAACACACCGCGCCG 420
|||||

DB 3055 TCTTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCAACACACCGCGCCG 3114
|||||

QY 421 TGAAGCTCGAGCTTTAAGGAGATTGCCAAGATTACGAAGTCGGTTTCGATTCGGTTGTGA 480
|||||

DB 3115 TGAAGCTCGAGCTTTAAGGAGATTGCCAAGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3174
|||||

QY 481 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGGAGTTTCTGAAT 540
|||||

DB 3175 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGGAGTTTCTGAAT 3234
|||||

QY 541 GCGCAGAGCAGAAATGCTGCCACGTGCTTCCGCGCGCGGTGGATTTCATGTTGGAGG 600
|||||

DB 3235 GCGCAGAGCAGAAATGCTGCCACGTGCTTCCGCGCGCGGTGGATTTCATGTTGGAGG 3294
|||||

QY 601 TTTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTAATTAAT 649
|||||

DB 3295 TTTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTAATTAAT 3354
|||||

QY 650 ----- 649

DB 3355 ACCATCTGCATTAAGCTATGTTTACACATTCAATGAATATGTTCTTACTGAGTACTTGTGA 3414
|||||

QY 650 -----TCAGAGGCACCTTATTTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 701
|||||

DB 3415 TTTGTTATTTACAGAGCAGCTTATTTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTG 3474
|||||

QY 702 GTTATACTCAAGCTTGCTTAATATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 761
|||||

DB 3475 GTTATACTCAAGCTTGCTTAATATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 3534
|||||

QY 762 AAAGAGATTATTTCAAGCTCTAATGTTAGATATGTTAGTCTTGAAGAGTCAATTCGCCGAA 821
|||||

DB 3535 AAAGAGATTATTTCAAGCTCTAATGTTAGATATGTTAGTCTTGAAGAGTCAATTCGCCGAA 3594
|||||

QY 822 GAGCTTTGTTAAAGAGATAATTTGATAGACGTAAGAGCTTGGTTTGGAGGTACCTTAAAGTA 881
|||||

DB 3595 GAGCTTTGTTAAAGAGATAATTTGATAGACGTAAGAGCTTGGTTTGGAGGTACCTTAAAGTA 3654
|||||

QY 882 AAGAAACATGTCGAAATGTACATAAGGCACTTGACTCGGATGATATGATGATGATGATGATGAT 941
|||||

DB 3655 AAGAAACATGTCGAAATGTACATAAGGCACTTGACTCGGATGATATGATGATGATGATGATGAT 3714
|||||

QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCTGCTCTTCAATTCGCTGTT 1001
|||||

DB 3715 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCTGCTCTTCAATTCGCTGTT 3774
|||||

QY 1002 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGATGTCAAC 1061
|||||

DB 3775 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGATGTCAAC 3834
|||||

QY 1062 CATAGGAATCCGAGGGATATACGGTGTCTCATGTTGCTGCGATCGGAGAGGCCACAA 1121
|||||

DB 3835 CATAGGAATCCGAGGGATATACGGTGTCTCATGTTGCTGCGATCGGAGAGGCCACAA 3894
|||||

QY 1122 TTGATACTATCTTATTCGAAAAAGGTGCAAGTGTCATCAGAAAGCAACTTTTGAAGGTAGA 1181
|||||

DB 3895 TTGATACTATCTTATTCGAAAAAGGTGCAAGTGTCATCAGAAAGCAACTTTTGAAGGTAGA 3954
|||||

QY 1182 ACCGCACTCATGATCGCAAAACAAAGCCACTATGGCGGTTGAATGTAATATATATATATATATAT 1241
|||||

DB 3955 ACCGCACTCATGATCGCAAAACAAAGCCACTATGGCGGTTGAATGTAATATATATATATATATAT 4014
|||||

xx This DNA encodes the Arabidopsis thaliana non-inducible immunity-1 (NIM1)
cc wild-type protein. This DNA can be mutated to produce altered forms of
cc the NIM1 protein. The invention provides a chimeric gene comprising a
cc promoter active in plants operatively linked to a DNA molecule that
cc encodes an altered form of the NIM1 protein. Plant cells stably
cc transformed with a recombinant vector comprising such a chimeric gene
cc have a broad spectrum of disease resistance. The altered NIM1 proteins
cc act as dominant-negative regulators of the systemic acquired resistance
cc (SAR) signal transduction pathway. The transgenic plants transformed with
cc an altered NIM1 gene exhibits constitutive SAR expression which is higher
cc in the transformed plants than in a wild-type plant. The products can be
cc used for producing plants with a broad spectrum disease resistance.
cc Overexpression of NIM1 mimics the effects of inducer compounds that
cc induce constitutive immunity (CIM) phenotype in plants. The inventions
cc can be used with plants such as rice, wheat, barley, rye, corn, potato,
cc carrot, sweet potato, sugar beet, bean, pea, chichory, lettuce, cabbage,
cc cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic,
cc eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber,
cc apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot,
cc strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya,
cc mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The
cc plants produced are resistant to plant pathogens such as viruses,
cc viroids, fungi, bacteria, insects such as aphids and lepidoptera and
cc nematodes. The plants produced can be used in agriculture.
xx Sequence 5655 BP; 1758 A; 1014 C; 1069 G; 1814 T; 0 other;

Query Match	83.7%;	Score	1760;	DB	19;	Length	5655;		
Best Local Similarity	87.5%;	Pred. No.	0;						
Matches	2088;	Conservative	0;	Mismatches	0;	Indels	298;	Gaps	3;
QY	1	TCGATCTTTAAACCAATCCAGTTGATAAGGCTCTCTCGTTGATTAGCAGAGATCTCTTTA	60						
DB	2695	TCGATCTTTAAACCAATCCAGTTGATAAGGCTCTCTCGTTGATTAGCAGAGATCTCTTTA	2754						
QY	61	ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCAATTCATGATTCGCCG	120						
DB	2755	ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACACCAATTCATGATTCGCCG	2814						
QY	121	ATTCCTTATGAATCAGCAGCACTAGTTCGCTCGGTACCGATAACACCACTCCTCTATTG	180						
DB	2815	ATTCCTTATGAATCAGCAGCACTAGTTCGCTCGGTACCGATAACACCACTCCTCTATTG	2874						
QY	181	TTTATCTGGCCGCCGAAACAGTACTCACCGGACCTGATGTATCTGCTGCAATTCGCTCT	240						
DB	2875	TTTATCTGGCCGCCGAAACAGTACTCACCGGACCTGATGTATCTGCTGCAATTCGCTCT	2934						
QY	241	CCAACAGCTTCGAATCCGCTCTTTGACTCCGCGGATGATTTCTACAGCAGCCTAAGCTTG	300						
DB	2935	CCAACAGCTTCGAATCCGCTCTTTGACTCCGCGGATGATTTCTACAGCAGCCTAAGCTTG	2994						
QY	301	TTCTCTCCGACGGCCGGGAAGTTCTTTCCACCGGTGGTTTTCTCAGCGAGAAGCTCTT	360						
DB	2995	TTCTCTCCGACGGCCGGGAAGTTCTTTCCACCGGTGGTTTTCTCAGCGAGAAGCTCTT	3054						
QY	361	TCCTTCAAGAGCGCTTTAGCCGCCGCTAAGAGAGAAAGACTCCAAACACACCGCCGCCG	420						
DB	3055	TCCTTCAAGAGCGCTTTAGCCGCCGCTAAGAGAGAAAGACTCCAAACACACCGCCGCCG	3114						
QY	421	TGAAGCTCAGACTTAAAGGAGATTGCGAAGGATTACGAAGTCGGTTTCGATTCGGTTTGA	480						
DB	3115	TGAAGCTCAGACTTAAAGGAGATTGCGAAGGATTACGAAGTCGGTTTCGATTCGGTTTGA	3174						
QY	481	CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCCTAAAGGAGTTTCTGAAT	540						
DB	3175	CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCCCTAAAGGAGTTTCTGAAT	3234						
QY	541	GGCAGACGAGAAATTCGTCGCCACGTGGCTTGCCGCCGCCGGTGGAATTCATGTTGGAGG	600						
DB	3235	GGCAGACGAGAAATTCGTCGCCACGTGGCTTGCCGCCGCCGGTGGAATTCATGTTGGAGG	3294						
QY	601	TTCTCTATTGGCTTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTAATTA	649						

DB	3295	TTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTAATTA	3354
QY	650	-----	649
DB	3355	ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATGTTCTTACTTGGATCTTGTA	3414
QY	650	-----TCAGAGGCACCTTATTGGACGCTGTGTAGACAAAGTTGTTATAGAGSACACATTG	701
DB	3415	TTTGTATTTCAGAGGCACCTTATTGGACGCTGTGTAGACAAAGTTGTTATAGAGSACACATTG	3474
QY	702	GTATATCTCAAGCTTGTCTTAATATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT	761
DB	3475	GTATATCTCAAGCTTGTCTTAATATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT	3534
QY	762	AAAGAGATTATTGTCAAGTCTAATGTAGATATGTTTAGTCTTGTAAAGTCAATTCGCCGAA	821
DB	3535	AAAGAGATTATTGTCAAGTCTAATGTAGATATGTTTAGTCTTGTAAAGTCAATTCGCCGAA	3594
QY	822	GAGCTTGTAAAGAGATAATTGATAGACCTAAAGAGCTTGTGTTGGAGTACCTAAAGTA	881
DB	3595	GAGCTTGTAAAGAGATAATTGATAGACCTAAAGAGCTTGTGTTGGAGTACCTAAAGTA	3654
QY	882	AGAAACATGCTCTCGAATGTACATAGGCACCTTGACTCGGATGATATTCAGTTAGTCAAG	941
DB	3655	AGAAACATGCTCTCGAATGTACATAGGCACCTTGACTCGGATGATATTCAGTTAGTCAAG	3714
QY	942	TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTCTCTTCATTTCCGCTGTT	1001
DB	3715	TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTCTCTTCATTTCCGCTGTT	3774
QY	1002	GCATATTGCAATGTGAAGACCCCAACAGATCTTTTAAACCTTGATCTTGCCCATGTCAAC	1061
DB	3775	GCATATTGCAATGTGAAGACCCCAACAGATCTTTTAAACCTTGATCTTGCCCATGTCAAC	3834
QY	1062	CATAGAAATCCGAGGGGATATACGGTGTCTCATGTTGCTGCGATCGGAGAGAGCCACAA	1121
DB	3835	CATAGAAATCCGAGGGGATATACGGTGTCTCATGTTGCTGCGATCGGAGAGAGCCACAA	3894
QY	1122	TTGATCTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA	1181
DB	3895	TTGATCTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGTAGA	3954
QY	1182	ACCGCACTCATGATCGCAAAACAGCCACTATGCGCGTGTGAATGTAATAATATCCCGGAG	1241
DB	3955	ACCGCACTCATGATCGCAAAACAGCCACTATGCGCGTGTGAATGTAATAATATCCCGGAG	4014
QY	1242	CAATGCAAGCATTTCTCTCAAGGCCGACTATGTGTAGAATACTAGAGCAAGAAGACAAA	1301
DB	4015	CAATGCAAGCATTTCTCTCAAGGCCGACTATGTGTAGAATACTAGAGCAAGAAGACAAA	4074
QY	1302	CGAGAACAAATTCCTAGAGATGTTCCCTCCTCTTTTGCAGTGGCGGCCGATGAATTTGAAG	1361
DB	4075	CGAGAACAAATTCCTAGAGATGTTCCCTCCTCTTTTGCAGTGGCGGCCGATGAATTTGAAG	4134
QY	1362	ATGACGCTGCTCGATCTTGAANAATAG	1387
DB	4135	ATGACGCTGCTCGATCTTGAANAATAGAGGTATCTATCAAGTCTTATTTCTTATATGTTTG	4194
QY	1388	-----	1387
DB	4195	AATTAATTTATGCTCTCTATTAGGAACCTGAGTGAACCTAATGATAACTATTTCTTTGT	4254
QY	1388	-----AGTTGCATTTGCTCAACGCTCTTTTCCACGGAAGCAGCAGCTGCA	1433
DB	4255	GTGCTCCACTGTTTAGTTGCACTTGTCTCAACGCTCTTTTCCACGGAAGCAGCAGCTGCA	4314
QY	1434	ATGAGATCCCGGAAATGAAGGAAACATGTAGTTCATAGTACTAGCCCTCGAGCCCTGAC	1493
DB	4315	ATGAGATCCCGGAAATGAAGGAAACATGTAGTTCATAGTACTAGCCCTCGAGCCCTGAC	4374
QY	1494	CGTCTCACTGGTAGAGAGAACATCACCGGGTGTAAAGATAGCAGCTTTTCAGAAATCTTA	1553

```
Db 4375 CGTCTACTGTAGAGAGAACATCACCGGTGTAAAGATAGCACCTTTTCAGAACTCTA 4434
Qy 1554 GAAGAGCATCAAGTAGACTAAAGCGCTTCTTAAACC----- 1592
Db 4435 GAAGAGCATCAAGTAGACTAAAGCGCTTCTTAAACC----- 4494
Qy 1593 ----- 1592
Db 4495 CATCGGACTCCTTATCACAAAAACAACTAAATGATCTTTAAACATGGTTTGTACT 4554
Qy 1593 -----GTGGAATCGGGAAACGATTTCTCCCGCGC 1622
Db 4555 TGCTGTCTGACTTGTGTTTTTTTATCATCAGTGGAACTCGGAAACGATTTCTCCCGCGC 4614
Qy 1623 TGTTCGGCAGTGCCTGACCACTGATGAGTGTGAGGACCTGACTCAACTGGCTTGGCGGA 1682
Db 4615 TGTTCGGCAGTGCCTGACCACTGATGAGTGTGAGGACCTGACTCAACTGGCTTGGCGGA 4674
Qy 1683 GAAGACGACACTGCTGAGAACGACTACAAAAGCAAGGATGATGGAATACAAAGAG 1742
Db 4675 GAAGACGACACTGCTGAGAACGACTACAAAAGCAAGGATGATGGAATACAAAGAG 4734
Qy 1743 ACACCTAAGAGGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCGTCCTCGACAGAT 1802
Db 4735 ACACCTAAGAGGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCGTCCTCGACAGAT 4794
Qy 1803 TCGACTTTCTCCACATCGAAATCAACCGGTGGAAGAGGCTTAACCGTAACCTCTCTCAT 1862
Db 4795 TCGACTTTCTCCACATCGAAATCAACCGGTGGAAGAGGCTTAACCGTAACCTCTCTCAT 4854
Qy 1863 CGTCGTCGGTGAGACTCTTCCTCTTAGTGTAAATTTTGTGCTGATACCATATAATTCGTGTT 1922
Db 4855 CGTCGTCGGTGAGACTCTTCCTCTTAGTGTAAATTTTGTGCTGATACCATATAATTCGTGTT 4914
Qy 1923 TCATGATGACTGTAACCTGTTTATGCTATCGTTGGCGTCAATAGTTTCGCTTTCGTTT 1982
Db 4915 TCATGATGACTGTAACCTGTTTATGCTATCGTTGGCGTCAATAGTTTCGCTTTCGTTT 4974
Qy 1983 TGCATCCTGTGTTATTTGCTGAGGTGCTGCTCAACAAATCTTCTAACAATTTGAACC 2042
Db 4975 TGCATCCTGTGTTATTTGCTGAGGTGCTGCTCAACAAATCTTCTAACAATTTGAACC 5034
Qy 2043 AATGGTATACAGATTGTTAATATATATTTATGTACATCAACATAA 2088
Db 5035 AATGGTATACAGATTGTTAATATATATTTATGTACATCAACATAA 5080
```

```
RESULT 8
AAV04632
ID AAV04632 standard; DNA; 5655 BP.
```

```
XX AAV04632;
```

```
AC XX
CT XX
DT 17-JUN-1998 (first entry)
```

```
XX Arabidopsis thaliana NIM1 gene.
```

```
DE Arabidopsis thaliana NIM1 gene.
XX NIM1; noninducible immunity; disease resistance; plants;
KW SAR gene expression; ss.
```

```
XX Arabidopsis thaliana.
```

```
XX
FH Key Location/Qualifiers
FT CDS 2787..4866)
FT FT /*tag= a "NIM1 protein"
FT FT /product= b
FT FT /tag= b
FT FT /number= 1
FT FT 3427..4162
FT FT /*tag= c
FT FT /number= 2
FT FT 4271..4474
FT FT exon
```

```
FT FT /*tag= d
FT FT /number= 3
FT FT 4586..4863
FT FT /*tag= e
FT FT /number= 4
XX
PN WO9749822-A1.
XX
XX 31-DEC-1997.
XX
XX 10-MAR-1997; 97WO-EP01218.
XX
XX 10-JAN-1997; 97US-0035022.
XX 21-JUN-1996; 96US-0020272.
XX 30-AUG-1996; 96US-0024883.
XX 13-DEC-1996; 96US-0033177.
XX 27-DEC-1996; 96US-0773559.
XX
XX (NOVS ) NOVARTIS AG.
XX
XX Delaney TP, Ellis DM, Friedrich LB, Johnson JE;
XX Lawton KA, Ryals JA, Weymann K;
XX
XX WPI; 1998-077185/07.
XX P-PSDB; AAW23963.
XX
XX NIM1 gene which allows activation in plant of systemic acquired
XX resistance - useful to confer broad spectrum disease resistance in
XX plants, specifically crop plants, e.g. rice, wheat, barley, rye and
XX corn
XX
XX Claim 2; Fig 15; 153pp; English.
XX
XX The sequence is that of the NIM1 (noninducible immunity) gene. It
XX may be used to confer a broad spectrum disease resistance in plants,
XX specifically crop plants, e.g. rice, wheat, barley, rye and corn.
XX The NIM1 gene can be used to confer universal disease susceptibility
XX to plant cells, and their progeny. It can also be used in a screening
XX method for identifying compounds capable of inducing broad spectrum
XX disease resistance in plants, while the plant cells, and their
XX progeny, can be used to isolate a gene fragment which allows
XX expression of broad spectrum disease resistance in plants, or to
XX incorporate the resistant trait into plant lines through breeding.
XX
XX Sequence 5655 BP; 1758 A; 1014 C; 1069 G; 1814 T; 0 other;
```

```
Query Match 83.7%; Score 1760; DB 19; Length 5655;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;
```

```
Qy 1 TCGATCTTTAACCAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60
Db 2695 TCGATCTTTAACCAATCCAGTTGATAAGGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 2754
Qy 61 ATTTGTGAATTTCAATTCATCGAACCTGTTGATGGACACCAACCATTCATGGATTCGCCG 120
Db 2755 ATTTGTGAATTTCAATTCATCGAACCTGTTGATGGACACCAACCATTCATGGATTCGCCG 2814
Qy 121 ATTCCTTATSAATCAGCAGCAGTCTAGTTTCGTCGTACCGATAACACCGACTCTCTATTG 180
Db 2815 ATTCCTTATSAATCAGCAGCAGTCTAGTTTCGTCGTACCGATAACACCGACTCTCTATTG 2874
Qy 181 TTTATCTGGCGCGGACAAAGTACTACCGGACCTGATGATGATCTGCTCTCAATTCGCTCT 240
Db 2875 TTTATCTGGCGCGGACAAAGTACTACCGGACCTGATGATGATCTGCTCTCAATTCGCTCT 2934
Qy 241 CCAACAGCTTCGAATCCGCTCTTTGACTCGCGGATGATTTCTACAGGACGCTCAAGCTTG 300
Db 2935 CCAACAGCTTCGAATCCGCTCTTTGACTCGCGGATGATTTCTACAGGACGCTCAAGCTTG 2994
Qy 301 TTTCTCTCGAGCGCGGGAAGTTTCTTTCCACCGGTGCGTTTTCAGCGGAGAGCTCTT 360
Db 2995 TTTCTCTCGAGCGCGGGAAGTTTCTTTCCACCGGTGCGTTTTCAGCGGAGAGCTCTT 3054
```

```
QY 361 TCTTCAAGACGCTTTAGCGCGCTAAGAGGAGAAAGACTCCAACAACACGCGCGCG 420
Db 3055 TCTTCAAGACGCTTTAGCGCGCGCTAAGAGGAGAAAGACTCCAACAACACGCGCGCG 3114
QY 421 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGTGA 480
Db 3115 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGTGA 3174
QY 481 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTAAAGAGATTTCGTAAT 540
Db 3175 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTAAAGAGATTTCGTAAT 3234
QY 541 GCGCAGACGAGATTGCTGCCAGTGTGCTTGCAGCGCGCGGTGGATTTCATGTTGAGG 600
Db 3235 GCGCAGACGAGATTGCTGCCAGTGTGCTTGCAGCGCGCGGTGGATTTCATGTTGAGG 3294
QY 601 TTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTA----- 649
Db 3295 TTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTAATCAGGTAATAAC 3354
QY 650 ----- 649
Db 3355 ACCATCTGCATTAAAGCTATGTTTACAAATTCATGAATATGTTCTTACTTGAGTACTGTA 3414
QY 650 -----TCAGAGGCACTTATTGGAGCTTGTAGACAAAGTTGTTATAGAGGACACATTG 701
Db 3415 TTTGATTTTCAGAGGCACTTATTGGAGCTTGTAGACAAAGTTGTTATAGAGGACACATTG 3474
QY 702 GTTATACTCAAGCTTGCTAATAATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 761
Db 3475 GTTATACTCAAGCTTGCTAATAATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 3534
QY 762 AAGAGATTAATGTCAGTCTAATGTAGATATGTTAGTCTTGAAAGATCATTTGCCGGAA 821
Db 3535 AAGAGATTAATGTCAGTCTAATGTAGATATGTTAGTCTTGAAAGATCATTTGCCGGAA 3594
QY 822 GAGCTTGTAAAGAGATAATTGATAGACGTTAAAGAGCTTGGTTTGGAGGTACCTTAAAGTA 881
Db 3595 GAGCTTGTAAAGAGATAATTGATAGACGTTAAAGAGCTTGGTTTGGAGGTACCTTAAAGTA 3654
QY 882 AAGAAACATGCTCGAATGTACATAAAGCAGCTTACGTCGGATGATATTGATTAGTCAAG 941
Db 3655 AAGAAACATGCTCGAATGTACATAAAGCAGCTTACGTCGGATGATATTGATTAGTCAAG 3714
QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTTCGCTGTT 1001
Db 3715 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTTCATTTTCGCTGTT 3774
QY 1002 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTGCAGATGTCAC 1061
Db 3775 GCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTGCAGATGTCAC 3834
QY 1062 CATAGGAATCCGAGGGATATACGGTCTTCATGTTGCTCGGATGCGGAGAGGCCACAA 1121
Db 3835 CATAGGAATCCGAGGGATATACGGTCTTCATGTTGCTCGGATGCGGAGAGGCCACAA 3894
QY 1122 TTGATCTATCTCTATTGGAAGAGGTGCAAGTGCATCAGAAGCACTTTTGAAGGTAGA 1181
Db 3895 TTGATCTATCTCTATTGGAAGAGGTGCAAGTGCATCAGAAGCACTTTTGAAGGTAGA 3954
QY 1182 ACCGCACTCATGATCGCAAAAACAAGCCACTATGCGGTTTGAATGTAATATATCCCGGAG 1241
Db 3955 ACCGCACTCATGATCGCAAAAACAAGCCACTATGCGGTTTGAATGTAATATATCCCGGAG 4014
QY 1242 CAATGCAGCATTTCTCTCAAGAGCGGACTATGCTAGAAATACTAGACGAGAGACAAA 1301
Db 4015 CAATGCAGCATTTCTCTCAAGAGCGGACTATGCTAGAAATACTAGACGAGAGACAAA 4074
QY 1302 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGATGAATTTGAAG 1361
Db 4075 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGATGAATTTGAAG 4134
```

```
QY 1362 ATGACGCTGCTCGATCTTTGAAATAG----- 1387
Db 4135 ATGACGCTGCTCGATCTTTGAAATAGAGGTATCTATCAAGTCTTATTCTTATATGTTG 4194
QY 1388 ----- 1387
Db 4195 AATTAAATTTATGTCCTCTCTATTAGGAACTGAGTGAACTAATGATAACTATTCTTTGT 4254
QY 1388 -----AGTTGCACCTTGCTCAAGCTCTTTTCCAAAGGAGACACAAGCTGCA 1433
Db 4255 GTCGTCACACTGTTTAGTTGCACCTGCTCAAGCTCTTTTCCAAAGGAGACACAAGCTGCA 4314
QY 1434 ATGGAGATCGCCGAATGAAGGGAACATGTGAGTTCATAGTACTAGCTCGAGCCTGAC 1493
Db 4315 ATGGAGATCGCCGAATGAAGGGAACATGTGAGTTCATAGTACTAGCTCGAGCCTGAC 4374
QY 1494 CGTCTCACTGTTACCAAGAGACATCACCGGTGTAAGATAGCACCTTTTCAGAAATCCTA 1553
Db 4375 CGTCTCACTGTTACCAAGAGACATCACCGGTGTAAGATAGCACCTTTTCAGAAATCCTA 4434
QY 1554 GAAGAGCATCAAGTAGACTTAAAGCGCTTTCTTAAACC----- 1592
Db 4435 GAAGAGCATCAAGTAGACTTAAAGCGCTTTCTTAAACC----- 1592
QY 1593 ----- 1592
Db 4495 CATCGGACTCCTTATCACAAAAACAACTAAATGATCTTTAAACATGGTTTGTACT 4554
QY 1593 -----GTGGAACTCGGGAAACGATTTCTCCCGCGC 1622
Db 4555 TGCTGTCTGACCTGTTTTTTTATCATCAGTGGAACTCGGAAACGATTTCTCCCGCGC 4614
QY 1623 TGTTCGGCAGTCTCGACAGATTATGAACCTGTGAGGACTTGACTCAACTGGCTTCCGGA 1682
Db 4615 TGTTCGGCAGTCTCGACAGATTATGAACCTGTGAGGACTTGACTCAACTGGCTTCCGGA 4674
QY 1683 GAAGAGCAGTCTGTGAGAAAGCAGCTACAAAAGAGCAAGGTACATGGAATACAAG 1742
Db 4675 GAAGAGCAGTCTGTGAGAAAGCAGCTACAAAAGAGCAAGGTACATGGAATACAAG 4734
QY 1743 ACATAAAGAGGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCGTCCTGACAGAT 1802
Db 4735 ACATAAAGAGGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTCGTCCTGACAGAT 4794
QY 1803 TGCATTTCTCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT 1862
Db 4795 TGCATTTCTCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT 4854
QY 1863 CGTCGTCGCTGAGACTCTTGCCTCTTAGTGTAAATTTTCTGCTGACCATATAATTTCTGTTT 1922
Db 4855 CGTCGTCGCTGAGACTCTTGCCTCTTAGTGTAAATTTTCTGCTGACCATATAATTTCTGTTT 4914
QY 1923 TCATGATGACTGTAACCTGTTTATGCTATCGTTGGCGTCATATAGTTTGGCTTCTGTTT 1982
Db 4915 TCATGATGACTGTAACCTGTTTATGCTATCGTTGGCGTCATATAGTTTGGCTTCTGTTT 4974
QY 1983 TGCATCCTGTGTATTATGCTGAGGTGCTTCAACAAGTGTGTACATTTGAAC 2042
Db 4975 TGCATCCTGTGTATTATGCTGAGGTGCTTCAACAAGTGTGTGTAAACAATTTGAACC 5034
QY 2043 AATGGTATACAGATTTGTAATATATATTTATGTACATCAACAATA 2088
Db 5035 AATGGTATACAGATTTGTAATATATATTTATGTACATCAACAATA 5080
```

RESULT 9
AAV43658/C
ID AAV43658 standard; DNA; 9919 BP.
XX
AC AAV43658;
XX
DT 29-SEP-1998 (first entry)
XX

DE A. thaliana non-inducible immunity-1 (NIM1) genomic sequence.

XX Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;
KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;
KW constitutive immunity; agriculture; ss.

XX Arabidopsis thaliana.

XX W09826082-A1.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-EP07012.

XX 20-JUN-1997; 97US-0880179.

XX 13-DEC-1996; 96US-0033177.

XX 27-DEC-1996; 96US-0034379.

XX 27-DEC-1996; 96US-0034382.

XX 10-JAN-1997; 97US-0034730.

XX 10-JAN-1997; 97US-0035021.

XX 10-JAN-1997; 97US-0035022.

XX (NOVS) NOVARTIS AG.

XX Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;

XX Uknes SJ;

XX WPI; 1998-348536/30.

XX Use of non-inducible immunity-1 gene - for transforming plants to
XX produce transgenic plants having a broad spectrum disease resistance

XX Example 11; Pages 98-107; 205pp; English.

XX This represents the genomic sequence of the Arabidopsis thaliana
CC non-inducible immunity-1 (NIM1) gene. The invention provides a chimeric
CC gene comprising a promoter active in plants operatively linked to a DNA
CC molecule that encodes an altered form of the NIM1 protein. Plant cells
CC stably transformed with a recombinant vector comprising such a chimeric
CC gene have a broad spectrum of disease resistance. The altered NIM1
CC proteins act as dominant-negative regulators of the systemic acquired
CC resistance (SAR) signal transduction pathway. The transgenic plants
CC transformed with an altered NIM1 gene exhibits constitutive SAR
CC expression which is higher in the transformed plants than in a wild-type
CC plant. The products can be used for producing plants with a broad
CC spectrum disease resistance. Overexpression of NIM1 mimics the effects
CC of inducer compounds that induce constitutive immunity (CIM) phenotype in
CC plants. The inventions can be used with plants such as e.g. rice, wheat,
CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
CC chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
CC tomato, sorghum and sugarcane. The plants produced are resistant to plant
CC pathogens such as viruses, viroids, fungi, bacteria, insects such as
CC aphids and lepidoptera and nematodes. The plants produced can be used in
CC agriculture.

XX Sequence 9919 BP; 3150 A; 1825 C; 1737 G; 3207 T; 0 other;

XX Query Match 83.7%; Score 1760; DB 19; Length 9919;
XX Best Local Similarity 87.5%; Pred. No. 0;
XX Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;

QY 1 TCGATCTTTAACCAATCCAGTTGATAGGCTCTTCCTGTTAGTAGCAGAGATCTCTTTA 60
DB TCGATCTTTAACCAATCCAGTTGATAGGCTCTTCCTGTTAGTAGCAGAGATCTCTTTA 3808

QY 61 ATTTGTGAATTCATTCGGAACCTGTTGATGGACACCAACCATTCATGGATTCGCCG 120

DB ATTTGTGAATTCATTCGGAACCTGTTGATGGACACCAACCATTCATGGATTCGCCG 3748

QY 121 ATTCTTATGAATCAGCAGCACTAGTTTTCGTCGTACCGATACACACGACTCCTCTATTG 180
DB TTTTATGAATCAGCAGCACTAGTTTTCGTCGTACCGATACACACGACTCCTCTATTG 3688
QY 181 TTTATCTGGCCGCGCAACAAGTACTCACCGGACTGATGTATCTGCTCTGCAATTCGCT 240
DB TTTATCTGGCCGCGCAACAAGTACTCACCGGACTGATGTATCTGCTCTGCAATTCGCT 3628
QY 241 CCAACAGCTTCGAATCCGCTCTTTGACTCGCCGAGATATTTCTACAGCAGCGCTAAGCTG 300
DB CCAACAGCTTCGAATCCGCTCTTTGACTCGCCGAGATATTTCTACAGCAGCGCTAAGCTG 3568
QY 301 TTCTCTCCGAGCGCGGGAAGTTTCTTTCCACCGGTCGCTTTTCTACGAGAGCTCTT 360
DB TTCTCTCCGAGCGCGGGAAGTTTCTTTCCACCGGTCGCTTTTCTACGAGAGAGCTCTT 3508
QY 361 TCTTCAAGAGCGCTTTAGCCGCCCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG 420
DB TCTTCAAGAGCGCTTTAGCCGCCCTAAGAAGGAGAAAGACTCCAACAACACCGCCGCCG 3448
QY 421 TGAAGCTCGAGCTTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 480
DB TGAAGCTCGAGCTTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3388
QY 481 CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCTTAAGGAGTTTCTGAAT 540
DB CTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCTTAAGGAGTTTCTGAAT 3328
QY 541 GCGCAGACGAGAATTGCTGCACGTTGCCGCGCGCGGCTGGATTTTCATGTTGGAGG 600
DB GCGCAGACGAGAATTGCTGCACGTTGCCGCGCGCGGCTGGATTTTCATGTTGGAGG 3268
QY 601 TTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTA 649
DB TTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTA 3208
QY 650 ----- 649
DB ACCATCTGCAATTAAGCTATGGTTACACATTCATGATATATGTTTACTTCAGTACTTGA 3148
QY 650 -----TCAGAGGCACTTATTGGAGCTGTAGACAAAGTTGTTATAGAGGACACATTG 701
DB TTTGTTATTTTCAGAGGCACTTATTGGAGCTGTAGACAAAGTTGTTATAGAGGACACATTG 3088
QY 702 GTTATCTCAAGCTTGTCTATATATGTTGTTAAAGCTTGTATGAAGCTATTTGGATAGATGT 761
DB GTTATCTCAAGCTTGTCTATATATGTTGTTAAAGCTTGTATGAAGCTATTTGGATAGATGT 3028
QY 762 AAGAGATTTATGTCAGTCTAATGTAGATATGTTAGTCTTGAAGTCAATTCGCCGAA 821
DB AAGAGATTTATGTCAGTCTAATGTAGATATGTTAGTCTTGAAGTCAATTCGCCGAA 2968
QY 822 GAGCTTCTTAAAGAGATAATTGATAGACGTTAAAGAGCTGTTGTTGGAGGTACCTAAAGTA 881
DB GAGCTTCTTAAAGAGATAATTGATAGACGTTAAAGAGCTGTTGTTGGAGGTACCTAAAGTA 2908
QY 882 AAGNAACATGTCGAATGTACATTAAGGCACTTGCCTCGGATGATATGATGATGATCAAG 941
DB AAGNAACATGTCGAATGTACATTAAGGCACTTGCCTCGGATGATATGATGATGATCAAG 2848
QY 942 TTGCTTTTGAAGAGGATCACCAATCTAGATGATGCTGCTCTTCAATTCGCTGTT 1001
DB TTGCTTTTGAAGAGGATCACCAATCTAGATGATGCTGCTCTTCAATTCGCTGTT 2788
QY 1002 GCATTTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTTCATCTTCCGATGTCAC 1061
DB GCATTTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTTCATCTTCCGATGTCAC 2728
QY 1062 CATAGGAATCCGAGGGGATATACGGTCTTCATGTTGCTCGGATGCGGAGGAGGACACAA 1121
DB CATAGGAATCCGAGGGGATATACGGTCTTCATGTTGCTCGGATGCGGAGGAGGACACAA 2668
QY 1122 TTGATACTATCTTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGGAGGTAGA 1181

Db 2667 TTGATCTATCTCTATTGGAAAAAGTGCAGTGCATCAGAAGCAACTTTTGGAGGTAGA 2608
Qy 1182 ACCGCACTCATGATCGAAACCAAGCCACTATGCGGTGTAATGTAATAATATATCCCGGAG 1241
Db 2607 ACCGCACTCATGATCGAAACCAAGCCACTATGCGGTGTAATGTAATAATATCCCGGAG 2548
Qy 1242 CAATGCAAGCAATCTCTCAAGGCGGACTATGTGTAGAAATAGTAGAGCAAGAGACAAA 1301
Db 2547 CAATGCAAGCAATCTCTCAAGGCGGACTATGTGTAGAAATAGTAGAGCAAGAGACAAA 2488
Qy 1302 CGAGAACAAATTCCTAGAGATGTCCTCCCTCTTTTCCAGTGCGGCGGATGAATTGAAG 1361
Db 2487 CGAGAACAAATTCCTAGAGATGTCCTCCCTCTTTTCCAGTGCGGCGGATGAATTGAAG 2428
Qy 1362 ATGAGCGTCTCGATCTTGAATAATG----- 1387
Db 2427 ATGAGCGTCTCGATCTTGAATAATGAGGTATCTATCAAGTCTTATTTCTTATATGTTG 2368
Qy 1388 ----- 1387
Db 2367 AATTAATAATTTATGCTCTCTCTATTAGGAACAGTGAAGTGAATGAATCTTTTGT 2308
Qy 1388 -----AGTGCATCTGCTCAACGCTCTTTTCCACGGAAGCACAAGCTGCA 1433
Db 2307 GTCGTCCACTGTTTAGTTGCACTTGCTCAACGCTCTTTTCCACGGAAGCACAAGCTGCA 2248
Qy 1434 ATGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCACTAGCTAGCCCTCGAGCCCTGAC 1493
Db 2247 ATGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCACTAGCTAGCCCTCGAGCCCTGAC 2188
Qy 1494 CGTCTCACTGTTAGTGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAAATCCTA 1553
Db 2187 CGTCTCACTGTTAGTGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAAATCCTA 2128
Qy 1554 GAAGAGCATCAAGTAGACTTAAGAGCGTTTCTAAAC----- 1592
Db 2127 GAAGAGCATCAAGTAGACTTAAGAGCGTTTCTAAACCGGTATGAGATTCTCACCCACTT 2068
Qy 1593 ----- 1592
Db 2067 CATCGGACTCTTATCACAAAAACAATAATGATCTTTAAACATGTTTGTACT 2008
Qy 1593 -----GTGGAACCTCGGGAACGATCTTCCCGCGC 1622
Db 2007 TCGTCTGACCTTGTTTTTTTATCATCACTGGAACCTCGGGAACGATCTTCCCGCGC 1948
Qy 1623 TGTTCGCAGTGTCTGACAGATTATGAACCTGTGAGACTTGACTCAACTGGCTTGCGBA 1682
Db 1947 TGTTCGCAGTGTCTGACAGATTATGAACCTGTGAGACTTGACTCAACTGGCTTGCGBA 1888
Qy 1683 GAAGACGACACTGCTGAGAAACGACTCAAAAGAAAGCAAGGTACATGGAATACAAGAG 1742
Db 1887 GAAGACGACACTGCTGAGAAACGACTCAAAAGAAAGCAAGGTACATGGAATACAAGAG 1828
Qy 1743 ACATTAAGAAGCGCTTTAGTAGAGACAAATTGGAATTAGGAATTCGTCCTCGACAGAT 1802
Db 1827 ACATTAAGAAGCGCTTTAGTAGAGACAAATTGGAATTAGGAATTCGTCCTCGACAGAT 1768
Qy 1803 TCGACTTCTCCACATCGAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT 1862
Db 1767 TCGACTTCTCCACATCGAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT 1708
Qy 1863 CGTCGTGGTGAGACTCTTGCTCTTATGTTGTAATTTTGTGTACCATATAATTTCTGTTT 1922
Db 1707 CGTCGTGGTGAGACTCTTGCTCTTATGTTGTAATTTTGTGTACCATATAATTTCTGTTT 1648
Qy 1923 TCATGAGACTGTAACTGTTTATGCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTTT 1982
Db 1647 TCATGAGACTGTAACTGTTTATGCTATCGTTGGCGTCATATAGTTTCGCTCTTCGTTT 1588
Qy 1983 TGCATCTCTGTATTATTGCTGCAAGGTGCTTCAACAAATGTTGTAACAAATTTGAACC 2042

Db 1587 TGCATCTCTGTATTATTGCTGCAGGTGCTTCAACAAATGTTGTAAACAATTTGAACC 1528
Qy 2043 AATGGTATACAGATTGTAAT 2088
Db 1527 AATGGTATACAGATTGTAAT 1482
RESULT 10
AAV04631/c
ID AAV04631 standard; DNA; 9919 BP.
XX AC AAV04631;
XX DT 17-JUN-1998 (first entry)
XX DE Arabidopsis thaliana BAC-04 containing the NIM1 gene.
KW NIM1; noninducible immunity; disease resistance; plants;
KW SAR gene expression; ss.
XX OS Arabidopsis thaliana.
XX PN W09749822-Al.
XX PD 31-DEC-1997.
XX PF 10-MAR-1997; 97WO-EP01218.
XX PR 10-JAN-1997; 97US-0035022.
XX PR 21-JUN-1996; 96US-0020272.
XX PR 30-AUG-1996; 96US-0024883.
XX PR 13-DEC-1996; 96US-0033177.
XX PR 27-DEC-1996; 96US-0773559.
XX PA (NOVS) NOVARTIS AG.
XX PI Delaney TP, Ellis DM, Friedrich LB, Johnson JE;
XX PI Lawton KA, Ryals JA, Weymann K;
XX WPI; 1998-077185/07.
XX NIM1 gene which allows activation in plant of systemic acquired
PT resistance - useful to confer broad spectrum disease resistance in
PT plants, specifically crop plants, e.g. rice, wheat, barley, rye and
PT corn
XX Claim 4; Fig 14; 153pp; English.
XX The sequence is that of the 9.9kb region of clone BAC-04 containing
CC the NIM1 (noninducible immunity) gene. It may be used to confer a
CC broad spectrum disease resistance in plants, specifically crop plants,
CC e.g. rice, wheat, barley, rye and corn. The NIM1 gene can be used to
CC confer universal disease susceptibility to plant cells, and their
CC progeny. It can also be used in a screening method for identifying
CC compounds capable of inducing broad spectrum disease resistance in
CC plants, while the plant cells, and their progeny, can be used to
CC isolate a gene fragment which allows expression of broad spectrum
CC disease resistance in plants, or to incorporate the resistant trait
CC into plant lines through breeding.
XX Sequence 9919 BP; 3150 A; 1826 C; 1737 G; 3206 T; 0 other;
SQ Query Match 83.7%; Score 1760; DB 19; Length 9919;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;
Qy 1 TCGATCTTTAAACCAATCCAGTTGATAGGTCTCTCGTTGATTAGCAGAGATCTTTTA 60
Db 3867 TCGATCTTTAAACCAATCCAGTTGATAGGTCTCTCGTTGATTAGCAGAGATCTTTTA 3808
Qy 61 ATTTGTGAATTTCAATTCATCGAACCTTTGATGGACACCACCATTTGATGATTTCGCCG 120
Db 3807 ATTTGTGAATTTCAATTCATCGAACCTTTGATGGACACCACCATTTGATGATTTCGCCG 3748

QY 121 ATTCTTATGAATCAGCAGCACTAGTTTCGTCCGTACCGATACACCGACTCCTCTATTG 180
DB 3747 ATTCTTATGAATCAGCAGCACTAGTTTCGTCCGTACCGATACACCGACTCCTCTATTG 3688
QY 181 TTTATCTGGCCGCGCAACAAGTACTACCGGACTGATGTATCTGCTCTCAATTTGCTCT 240
DB 3687 TTTATCTGGCCGCGCAACAAGTACTACCGGACTGATGTATCTGCTCTCAATTTGCTCT 3628
QY 241 CCAACAGCTTCGAATTCGGTCTTGACTCGCGGGATGATTTCTACAGCGACGCTTAAGCTTG 300
DB 3627 CCAACAGCTTCGAATTCGGTCTTGACTCGCGGGATGATTTCTACAGCGACGCTTAAGCTTG 3568
QY 301 TTCTCTCCGAGCGCGGAAGTTTCTTCCACCGGTGCGTTTTGTACGCGAGAGCTCTT 360
DB 3567 TTCTCTCCGAGCGCGGAAGTTTCTTCCACCGGTGCGTTTTGTACGCGAGAGCTCTT 3508
QY 361 TCTTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCAACAACACCGCGCGCG 420
DB 3507 TCTTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCCAACAACACCGCGCGCG 3448
QY 421 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 480
DB 3447 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3388
QY 481 CTGTTTTGGCTTATGTTTACAGCAGCAGCTGAGACCGCGCCTAAAGGAGTTTCTCGAAT 540
DB 3387 CTGTTTTGGCTTATGTTTACAGCAGCAGCTGAGACCGCGCCTAAAGGAGTTTCTCGAAT 3328
QY 541 GCGCAGACGAGAATTGCTGCCAGCTGGCTTGCCGCGCGCGGGTGGATTTTCATGTTGGAGG 600
DB 3327 GCGCAGACGAGAATTGCTGCCAGCTGGCTTGCCGCGCGCGGGTGGATTTTCATGTTGGAGG 3268
QY 601 TTCTCTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTA----- 649
DB 3267 TTCTCTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTAAGGTAATAA 3208
QY 650 ----- 649
DB 3207 ACCATCTGCATTAAAGCTATGTTACACATTCATGAATATGTTCTTACTTGAAGTACTGTA 3148
QY 650 -----TCAGAGGCACTTATTTGGAGTGTAGACAAAGTTGTTATAGAGGACACATTG 701
DB 3147 TTTGTATTTTCAGAGGCACTTATTTGGAGTGTAGACAAAGTTGTTATAGAGGACACATTG 3088
QY 702 GTTATACTCAAGCTTGTCTAATATATGTGTAAGCTTGTATGAAGCTATTTGATAGATGT 761
DB 3087 GTTATACTCAAGCTTGTCTAATATATGTGTAAGCTTGTATGAAGCTATTTGATAGATGT 3028
QY 762 AAAGAGATTATTGCTCAAGTCTAATGTAGATATGTTTAGTCTTGAAGAAGTCATTGCCGGA 821
DB 3027 AAAGAGATTATTGCTCAAGTCTAATGTAGATATGTTTAGTCTTGAAGAAGTCATTGCCGGA 2968
QY 822 GAGCTTGTAAAGAGATAATTGTATAGACGTAAAGAGCTTGGTTGGAGGTACCTAAAGTA 881
DB 2967 GAGCTTGTAAAGAGATAATTGTATAGACGTAAAGAGCTTGGTTGGAGGTACCTAAAGTA 2908
QY 882 AAGAAACATGCTCGAATGTACATAAGGCACTTGACTCGSATGATATGAGTTAGTTAGTCAAG 941
DB 2907 AAGAAACATGCTCGAATGTACATAAGGCACTTGACTCGSATGATATGAGTTAGTTAGTCAAG 2848
QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGGTGCTCTTTCATTTCCGCTGTT 1001
DB 2847 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGGTGCTCTTTCATTTCCGCTGTT 2788
QY 1002 GCATATTCNAATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTTCCGATGTCAAC 1061
DB 2787 GCATATTCNAATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTTCCGATGTCAAC 2728
QY 1062 CATAGGAATCCGAGGGATATAGGTTTCATGTTGCTGCCATGCGGAAGGAGGCACAA 1121
DB 2727 CATAGGAATCCGAGGGATATAGGTTTCATGTTGCTGCCATGCGGAAGGAGGCACAA 2668

QY 1122 TTGATACTATCTCTATTGGAAGAGTGCAGTGCATCAGAAGCAACTTTTGAAGGTAGA 1181
DB 2667 TTGATACTATCTCTATTGGAAGAGTGCAGTGCATCAGAAGCAACTTTTGAAGGTAGA 2608
QY 1182 ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCGGAG 1241
DB 2607 ACCGCACTCATGATCGCAAAACAAGCCACTATGGCGGTTGAATGTAATAATATCCGGAG 2548
QY 1242 CAATGCAAGCATTTCTCTCAAGGCGGACTATGTGTAGAAATACTAGAGCAAGACACAAA 1301
DB 2547 CAATGCAAGCATTTCTCTCAAGGCGGACTATGTGTAGAAATACTAGAGCAAGACACAAA 2488
QY 1302 CGAGAACAAATTCCTTAGAGATGTTCCCTCCTCTTTTGCAGTGGCGCGCATGAATTTGAAG 1361
DB 2487 CGAGAACAAATTCCTTAGAGATGTTCCCTCCTCTTTTGCAGTGGCGCGCATGAATTTGAAG 2428
QY 1362 ATGAGCTCCTCGATCTTGGAAATAG----- 1387
DB 2427 ATGAGCTCCTCGATCTTGGAAATAGAGGTATCTATCAAGCTTATTTCTTATATGTTTG 2368
QY 1388 ----- 1387
DB 2367 AATTAATTTATGCTCCTCTCTATTAGGAACTGAGTGAACATAATGATAACTATTCTTTGT 2308
QY 1388 -----AGTTGCACCTTCTCAACGCTCTTTTCCAACGGAAGCAAGCTGCA 1433
DB 2307 GTCGTCCACTGTTTATGTTGCACCTTCTCAACGCTCTTTTCCAACGGAAGCAAGCTGCA 2248
QY 1434 ATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCTCGAGCTGAC 1493
DB 2247 ATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCTCGAGCTGAC 2188
QY 1494 COTCTACTGTGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAACTCTA 1553
DB 2187 COTCTACTGTGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAACTCTA 2128
QY 1554 GAAGAGCATCAAGTAGACTTAAAGCGCTTCTTAAACC----- 1592
DB 2127 GAAGAGCATCAAGTAGACTTAAAGCGCTTCTTAAACCAGGTATGATGTTCTCACCCACTT 2068
QY 1593 ----- 1592
DB 2067 CATCGGACTCCTTATCACAAAAACAACATAAATGATCTTTAAACATGGTTTGTACT 2008
QY 1593 -----GTGGAACCTCGGGAACAGATCTTCCCGGC 1622
DB 2007 TGCTGTCTGACCTGTTTTTTTTTATCATCAGTGGAACTCGGGAACGATCTTCCCGGC 1948
QY 1623 TGTTCGGCAGTGTCTGACAGATTATGAACGTGTGAGGACTTGACTCAACTGGCTTGGGA 1682
DB 1947 TGTTCGGCAGTGTCTGACAGATTATGAACGTGTGAGGACTTGACTCAACTGGCTTGGGA 1888
QY 1683 GAAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGTACATGGAATACAAAG 1742
DB 1887 GAAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGTACATGGAATACAAAG 1828
QY 1743 ACACATAAGAGGCTTTAGTAGAGACAAATTTGGAATTAGGAAATTCGTCCTGACAGAT 1802
DB 1827 ACACATAAGAGGCTTTAGTAGAGACAAATTTGGAATTAGGAAATTCGTCCTGACAGAT 1768
QY 1803 TCGACTTCTCCACATCGAAATCAACGGTGAAGAGTCTAACCGTAAACTCTTCAT 1862
DB 1767 TCGACTTCTCCACATCGAAATCAACGGTGAAGAGTCTAACCGTAAACTCTTCAT 1708
QY 1863 CGTCGTGGTGAGACTCTTGCTCTTACTGTAATTTTTTGTGTACCATATATATTTCTGTTT 1922
DB 1707 CGTCGTGGTGAGACTCTTGCTCTTACTGTAATTTTTTGTGTACCATATATATTTCTGTTT 1648
QY 1923 TCATGATGACTGTAACTGTTTATGCTATCCTTGGCGTCATATAGTTTCGCTTCGTTT 1982
DB 1647 TCATGATGACTGTAACTGTTTATGCTATCCTTGGCGTCATATAGTTTCGCTTCGTTT 1588
QY 1983 TGCATCCTGTGTAATTATTGCTGCAGGTGCTTCAACAAATGTTGTAAACAAATTTGAAC 2042

[illegible]

```
Qy 1182 ACCGACTCATGATCGCAAAACAGCCACTATGCGGCTTGAATGTAATAATATATCCCGGAG 1241
Db 3961 ACCGACTCATGATCGCAAAACAGCCACTATGCGGCTTGAATGTAATAATATATCCCGGAG 4020
Qy 1242 CAATGCAAGCAATCTCTCAAGGCCGACTATGTAGAAAATCTAGAGCAAGAAGACAAA 1301
Db 4021 CAATGCAAGCAATCTCTCAAGGCCGACTATGTAGAAAATCTAGAGCAAGAAGACAAA 4080
Qy 1302 CGAGAACAAATCTCTAGAGATGTTCCCTCCCTCTTTTCAGTGGCGGCGGATGAATGAAG 1361
Db 4081 CGAGAACAAATCTCTAGAGATGTTCCCTCCCTCTTTTCAGTGGCGGCGGATGAATGAAG 4140
Qy 1362 ATGACGCTGCTCGATCTTTGAAAATAG----- 1387
Db 4141 ATGACGCTGCTCGATCTTTGAAAATAGAGGTATCTATCAAGCTCTATTCTTATATGTTTG 4200
Qy 1388 ----- 1387
Db 4201 AATTAAATTTATGTCCTCTCTATTAGGAAACTGAGTGAACATAATGATACTATTCTTTGT 4260
Qy 1388 -----AGTTGCACTTGCTCAACGCTCTTTTCCACGGAAGCACAAAGCTGCA 1433
Db 4261 GTCGTCACACTGTTAGTTGCACTTGCTCAACGCTCTTTTCCACGGAAGCACAAAGCTGCA 4320
Qy 1434 ATGAGATCGCCGAAATGAAGGAACATGTAGTTCATAGTACTGACCTCGAGCCTGAC 1493
Db 4321 ATGAGATCGCCGAAATGAAGGAACATGTAGTTCATAGTACTGACCTCGAGCCTGAC 4380
Qy 1494 CGTCTCACTGGTAGAGAGAACATCACCGGGTGTAAAGATAGACCTTTCAGAAATCCTA 1553
Db 4381 CGTCTCACTGGTAGAGAGAACATCACCGGGTGTAAAGATAGACCTTTCAGAAATCCTA 4440
Qy 1554 GAAGAGCATCAAGTATGACTTAAAGCGCTTCTTAAACCC----- 1592
Db 4441 GAAGAGCATCAAGTATGACTTAAAGCGCTTCTTAAACCCGGTATGATTCACCCACTT 4500
Qy 1593 ----- 1592
Db 4501 CATCGGACTCCTTATCACAAAAACAAACTAAATGATCTTTAAACATGTTTGTACT 4560
Qy 1593 -----GTGGAATCGGGAAACGATCTTCCCGCGCT 1623
Db 4561 TGCTGCTGACCTTGTTTTTTTATCATGAGTGAACCTCGGAAACGATCTTCCCGCGCT 4620
Qy 1624 GTTCGGCAGTGCACGACGATTATGAACCTGAGGACTTGACTCAACTGGCTTGGGAG 1683
Db 4621 GTTCGGCAGTGCACGACGATTATGAACCTGAGGACTTGACTCAACTGGCTTGGGAG 4680
Qy 1684 AAGACGACTGCTG-AGAAACGACTACAAAAGAACAAAGGTACATGGAATACAAAGAG 1742
Db 4681 AAGACGACTGCTGGAAGAACGACTACAAAAGAACAAAGGTACATGGAATACAAAGAG 4740
Qy 1743 ACATAAAGAGGCTTTAGTAGGACAAATTTGGAATTAGGAATTCGTCCTCGACAGAT 1802
Db 4741 ACATAAAGAGGCTTTAGTAGGACAAATTTGGAATTAGGAATTCGTCCTCGACAGAT 4800
Qy 1803 TCGACTTCTTCCACATCGAAATCAACGGTGGAAAGAGTCTAACCGTAAACTCTCTCAT 1862
Db 4801 TCGACTTCTTCCACATCGAAATCAACGGTGGAAAGAGTCTAACCGTAAACTCTCTCAT 4860
Qy 1863 CGTCGCGGTGAGACTCTTCCCTCTTAGTGTAATTTTGTGTACCATATAATCTCTGTTT 1922
Db 4861 CGTCGCGGTGAGACTCTTCCCTCTTAGTGTAATTTTGTGTACCATATAATCTCTGTTT 4920
Qy 1923 TCATGATGACTGTAACCTGTTTATGCTATGCTTGGCGGTCAATATAGTTTCGCTTCGTTT 1982
Db 4921 TCATGATGACTGTAACCTGTTTATGCTATGCTTGGCGGTCAATATAGTTTCGCTTCGTTT 4980
Qy 1983 TGCATCTGCTGTTATTATGCTGAGGTGCTTCAACAAATGTTTCACAATTTGAACC 2042
Db 4981 TGCATCTGCTGTTATTATGCTGAGGTGCTTCAACAAATGTTTCACAATTTGAACC 5040
Qy 2043 AATGGTATACAGATTTGTAATATATATTTATGATACATCAACAATAA 2088
```

```
Db 5041 AATGGTATACAGATTTGTAATATATATTTATGATACATCAACAATAA 5086
```

RESULT 12

AAV46277

ID AAV46277 standard: cDNA; 1608 BP.

XX AC AAV46277;

XX DT 16-OCT-1998 (first entry)

XX DE A. thaliana C-terminal truncated NIM-1 variant cDNA.

XX KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.

XX OS Arabidopsis thaliana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT CDS 43..1608

FT /*tag= a

FT /product= NIM-1

XX PN WO9829537-A2.

XX PD 09-JUL-1998.

XX PF 23-DEC-1997; 97WO-EP07253.

XX PR 10-JAN-1997; 97US-0035024.

XX PR 27-DEC-1996; 96US-0034378.

XX PA (NOVS) NOVARTIS AG.

XX PI Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;

XX DR WPI; 1998-388119/33.

XX DR P-PSDB; AAW64438.

XX PT Protection of immunomodulated plants against pathogens - comprises
XX applying microbicide to provide increase in resistance

XX PS Claim 17; Page 129-132; 164pp; English.

XX This sequence encodes a truncated variant NIM-1 protein from Arabidopsis
CC thaliana. This protein is used in a method resulting in the protection of
CC an immunomodulated plant having a first level of resistance and involves
CC treatment with at least 1 microbicide that confers a second level of
CC resistance, such that the plants have a third level of resistance greater
CC than the sum of the first two levels. The method can be applied to a wide
CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
CC against viruses, fungi, bacteria, insects and nematodes. The method
CC provides a high level of resistance and allows a reduction in the amount
CC of microbicide used. Since the process involves two different methods of
CC protection, it is unlikely that the pathogen will develop resistance to
CC the treatment.

XX SQ Sequence 1608 BP; 447 A; 340 C; 385 G; 436 T; 0 other;

Query Match 76.3%; Score 1605; DB 19; Length 1608;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GATCTCTTTAATTTCTGAATTTCAATTCGGAACCTGTTGATGGACACCAACCATGAT 110

Db 1 GATCTCTTTAATTTCTGAATTTCAATTCGGAACCTGTTGATGGACACCAACCATGAT 60

Qy 111 GGATTTCGCCGATTCCTTATGAATCAGCAGCACTAGTTTCGTCGGTACCGATAACACCGAC 170

Db 61 GGATTTCGCCGATTCCTTATGAATCAGCAGCACTAGTTTCGTCGGTACCGATAACACCGAC 120

QY 171 TCCTCTATTGTTTATCTGCGCGCGAACAAGTACTCACCGGACCTGATGTAATCTGCTCTG 230
Db 121 TCCTCTATTGTTTATCTGCGCGCGAACAAGTACTCACCGGACCTGATGTAATCTGCTCTG 180
QY 231 CAATTGCTCTCCAACAGCTTCGAATCCGCTTTGACTCGCGCGATGATTTCTACAGCGAC 290
Db 181 CAATTGCTCTCCAACAGCTTCGAATCCGCTTTGACTCGCGCGATGATTTCTACAGCGAC 240
QY 291 GCTAAGCTTGTCTCTCGAGCGCGGGAAGTTTCTTTCCACGGTGCGTTTGTTCAGCG 350
Db 241 GCTAAGCTTGTCTCTCGAGCGCGGGAAGTTTCTTTCCACGGTGCGTTTGTTCAGCG 300
QY 351 AGAAGCTCTTTCTTCAAGACGCTTTAGCGCGCTTAAGAAGAGAGAAACACTCCCAACAC 410
Db 301 AGAAGCTCTTTCTTCAAGACGCTTTAGCGCGCTTAAGAAGAGAGAAACACTCCCAACAC 360
QY 411 ACCGCGCGCTGAAGCTTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCTGGTTTCGAT 470
Db 361 ACCGCGCGCTGAAGCTTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCTGGTTTCGAT 420
QY 471 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAAGCA 530
Db 421 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAAGCA 480
QY 531 GTTCTGAATGCCGACAGAGAAATGCTGCCAGCTGGCTTGGCGCGCGGCTGGAATTC 590
Db 481 GTTCTGAATGCCGACAGAGAAATGCTGCCAGCTGGCTTGGCGCGCGGCTGGAATTC 540
QY 591 ATGTTGGAGTCTCTATTGCGCTTCATCTCAAGATCCCTGAATTAATCTCTCTAT 650
Db 541 ATGTTGGAGTCTCTATTGCGCTTCATCTCAAGATCCCTGAATTAATCTCTCTAT 600
QY 651 CAGAGCGACTTATGGACGTTGTAGACAAGTTGTTATAGAGACACATGTTGTTATACTC 710
Db 601 CAGAGCGACTTATGGACGTTGTAGACAAGTTGTTATAGAGACACATGTTGTTATACTC 560
QY 711 AAGCTTGCTAATATATGTGTAAGCTTGTATGAAGCTATTGATAGATGTAAAGAGATT 770
Db 661 AAGCTTGCTAATATATGTGTAAGCTTGTATGAAGCTATTGATAGATGTAAAGAGATT 720
QY 771 ATTGTCAGTCTAATGTAGATATGGTGTAGTCTTGAAGTCAATGCGGAGAGCTTGT 830
Db 721 ATTGTCAGTCTAATGTAGATATGGTGTAGTCTTGAAGTCAATGCGGAGAGCTTGT 780
QY 831 AAAGAGATAATTGATAGACATAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACAT 890
Db 781 AAAGAGATAATTGATAGACATAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACAT 840
QY 891 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950
Db 841 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 900
QY 951 AAAGAGGATCACACCAATCTAGATGATGCGTGTCCTTCATTTCCGCTGTTGCATATTGC 1010
Db 901 AAAGAGGATCACACCAATCTAGATGATGCGTGTCCTTCATTTCCGCTGTTGCATATTGC 960
QY 1011 AATGTGAAGACCGCAACAGATCTTTTAAAACTTGTATCTTGGCGATGTCAACCATAGGAAT 1070
Db 961 AATGTGAAGACCGCAACAGATCTTTTAAAACTTGTATCTTGGCGATGTCAACCATAGGAAT 1020
QY 1071 CCGAGGGGATATACGGTGTCTCATGTCTGCGATGCGGAGAGCCACCAATGATACTA 1130
Db 1021 CCGAGGGGATATACGGTGTCTCATGTCTGCGATGCGGAGAGCCACCAATGATACTA 1080
QY 1131 TCTCTATTGGAAGAGGTGCAAGTGCAATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1190
Db 1081 TCTCTATTGGAAGAGGTGCAAGTGCAATCAGAAGCAACTTTGGAAGGTAGAACCGCACTC 1140
QY 1191 ATGATCGCAAAACAGCCACTATGGCGGTTGAATGTAATATATCCGGAGCAATCGAAG 1250
Db 1141 ATGATCGCAAAACAGCCACTATGGCGGTTGAATGTAATATATCCGGAGCAATCGAAG 1200

QY 1251 CATTTCTCTCAAAGCGGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACA 1310
Db 1201 CATTTCTCTCAAAGCGGACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACA 1260
QY 1311 ATTCTTAGAGATGTTCTCCCTCTTTTGCAGTGGCGCGGATGAATTTGAAGATGACGCTG 1370
Db 1261 ATTCTTAGAGATGTTCTCCCTCTTTTGCAGTGGCGCGGATGAATTTGAAGATGACGCTG 1320
QY 1371 CTCGATCTTGAATAAGATGAGTTGCACCTTGTCTCAACGTCTTTTCCAAACGGAAGCACAAAGCT 1430
Db 1321 CTCGATCTTGAATAAGATGAGTTGCACCTTGTCTCAACGTCTTTTCCAAACGGAAGCACAAAGCT 1380
QY 1431 GCAATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTCATAGTACTAGCCTCGAGCCT 1490
Db 1381 GCAATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTCATAGTACTAGCCTCGAGCCT 1440
QY 1491 GACCGTCTCACTGGTACGAAGAGAACATCACCGGCTGTAAAGATAGCACCTTTTCAGAAATC 1550
Db 1441 GACCGTCTCACTGGTACGAAGAGAACATCACCGGCTGTAAAGATAGCACCTTTTCAGAAATC 1500
QY 1551 CTAGAAGAGCATCAAGTAGACTTAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGA 1610
Db 1501 CTAGAAGAGCATCAAGTAGACTTAAAGCGCTTTCTAAACCGTGGAACTCGGGAACGA 1560
QY 1611 TTCTTCCCGCGCTGTGCGCAGTGTCTGACACAGATTAATGAACCTGT 1655
Db 1561 TTCTTCCCGCGCTGTGCGCAGTGTCTGACACAGATTAATGAACCTGT 1605

RESULT 13

AAV43663
ID AAV43663 standard; cDNA; 1608 BP.

XX AC AAV43663;

XX DT 29-SEP-1998 (first entry)

XX DE Non-inducible immunity-1 (NIM1) protein variant 3 encoding cDNA.

XX KW Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;

XX KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;

XX KW constitutive immunity; agriculture; variant; ss.

XX OS Arabidopsis thaliana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT CDS 43..1608

XX FT /*tag= a

XX FT /product= "NIM1 protein variant 3"

XX FT /note= "C-terminal deletion compared to wild-type

XX FT NIM1 sequence"

XX PN W09826082-Al.

XX PD 18-JUN-1998.

XX PF 12-DEC-1997; 97WO-EP07012.

XX PR 20-JUN-1997; 97US-0880179.

XX PR 13-DEC-1996; 96US-0033177.

XX PR 27-DEC-1996; 96US-0034379.

XX PR 27-DEC-1996; 96US-0034382.

XX PR 10-JAN-1997; 97US-0034730.

XX PR 10-JAN-1997; 97US-0035021.

XX PR 10-JAN-1997; 97US-0035022.

XX PA (NOVS) NOVARTIS AG.

XX PI Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;

XX PI Uknes SJ;

XX WI WPI; 1998-348536/30.

DR P-PSDB; AAW61985.
XX use of non-inducible immunity-1 gene - for transforming plants to
PT produce transgenic plants having a broad spectrum disease resistance
XX
XX Claim 12; Pages 155-159; 205pp; English.
XX
CC This cDNA encodes an altered form of the Arabidopsis thaliana non-
CC inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
CC AAV43665 represent variants of the NIM1 cDNA. The invention provides a
CC chimeric gene comprising a promoter active in plants operatively linked
CC to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
CC cells stably transformed with a recombinant vector comprising such a
CC chimeric gene have a broad spectrum of disease resistance. The altered
CC NIM1 proteins act as dominant-negative regulators of the systemic
CC acquired resistance (SAR) signal transduction pathway. The transgenic
CC plants transformed with an altered NIM1 gene exhibits constitutive SAR
CC expression which is higher in the transformed plants than in a wild-type
CC plant. The products can be used for producing plants with a broad
CC spectrum disease resistance. Overexpression of NIM1 mimics the effects
CC of inducer compounds that induce constitutive immunity (CIM) phenotype
CC in plants. The inventions can be used with plants such as rice, wheat,
CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
CC chichory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry, tobacco,
CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
CC tomato, sorghum and sugarcane. The plants produced are resistant to
CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such
CC as aphids and lepidoptera and nematodes. The plants produced can be used
CC in agriculture.
XX
SQ Sequence 1608 BP; 447 A; 340 C; 385 G; 436 T; 0 other;
Query Match 76.3%; Score 1605; DB 19; Length 1608;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51 GATCTCTTAATTCGTAATTCATTCGACCTGGACCTGGTGTGAGCACCCATTCAT 110
DB 1 GATCTCTTAATTCGTAATTCATTCGGAACCTGGTGTGAGCACCCATTCAT 60
QY 111 GGATTCGCCGATTCCTATGAATCAGCAGCACTAGTTCGTCGCTACCGATAACACCGAC 170
DB 61 GGATTCGCCGATTCCTATGAATCAGCAGCACTAGTTCGTCGCTACCGATAACACCGAC 120
QY 171 TCCTCTATTTGTTATCTGCGCCCGAACAAGTACTCAGCGACCTGATGTAATCTGCTCTG 230
DB 121 TCCTCTATTTGTTATCTGCGCCCGAACAAGTACTCAGCGACCTGATGTAATCTGCTCTG 180
QY 231 CAATTGCTCTCAACAGCTTCGAATCCGCTCTTTGACTCGCCGGATGATTTCTACAGCGAC 290
DB 181 CAATTGCTCTCAACAGCTTCGAATCCGCTCTTTGACTCGCCGGATGATTTCTACAGCGAC 240
QY 291 GCTAAGCTTTGCTCTCCGACGGCGGAAGTTCTTTCCACCGGTGCGTTTGTCTGACG 350
DB 241 GCTAAGCTTTGCTCTCCGACGGCGGAAGTTCTTTCCACCGGTGCGTTTGTCTGACG 300
QY 351 AGAAGCTCTTTCTCAAGACGCTTTAGCCGCGCTAAGAAGGAGAAAGACTCCCAACAAC 410
DB 301 AGAAGCTCTTTCTCAAGACGCTTTAGCCGCGCTAAGAAGGAGAAAGACTCCCAACAAC 360
QY 411 ACCGCCGCGTGAAGCTGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 470
DB 361 ACCGCCGCGTGAAGCTGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGAT 420
QY 471 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGTGAGACCGCCGCTTAAGGA 530
DB 421 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGTGAGACCGCCGCTTAAGGA 480
QY 531 GTTCTCGAATGCCAGCAGAAATTCGCCACGTGGCTTCCCGCGCGGGTGGATTC 590
|||||

DB 481 GTTCTGAATGCGCAGACGAGAAATGCTGCCACGTGGCTTCCCGCGCGGGTGAATTC 540
QY 591 ATGTTGGAGGTTCTCTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTTACTTCTCTAT 650
DB 541 ATGTTGGAGGTTCTCTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTTACTTCTCTAT 600
QY 651 CAGAGGCACTTATTTGGACGTTGTAGACAAAGTTGTATAGAGAGACATTTGGTTTATACT 710
DB 601 CAGAGGCACTTATTTGGACGTTGTAGACAAAGTTGTATAGAGAGACATTTGGTTTATACT 660
QY 711 AAGCTTGCTTAATATATGTTGTAAGCTTGTATGAAGCTTATTTGAAGCTTATTTGAAGAGATT 770
DB 661 AAGCTTGCTTAATATATGTTGTAAGCTTGTATGAAGCTTATTTGAAGCTTATTTGAAGAGATT 720
QY 771 ATTGCAAGTCTAATGTAGATATGGTTAGTCTTTGAAAGTCAITTCGCGGAGAGACTTTGTT 830
DB 721 ATTGCAAGTCTAATGTAGATATGGTTAGTCTTTGAAAGTCAITTCGCGGAGAGACTTTGTT 780
QY 831 AAGAGATAATTTAGATAGACGTAAGACGTTGGTTGGAGGTACCTAAAGTAAAGAAACAT 890
DB 781 AAGAGATAATTTAGATAGACGTAAGACGTTGGTTGGAGGTACCTAAAGTAAAGAAACAT 840
QY 891 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTTAGTTCAGTTCGTTTGTG 950
DB 841 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTTAGTTCAGTTCGTTTGTG 900
QY 951 AAGAGGATCACACCAATCTAGATGATCGGTGCTCTCTTCATTTTCGCTGTTGCAATATGC 1010
DB 901 AAGAGGATCACACCAATCTAGATGATCGGTGCTCTCTTCATTTTCGCTGTTGCAATATGC 960
QY 1011 AATGTGAAGACCGCAACAGATCTTTTAAACTTTGATCTTTGCCGATGTCAACCATAGGAAT 1070
DB 961 AATGTGAAGACCGCAACAGATCTTTTAAACTTTGATCTTTGCCGATGTCAACCATAGGAAT 1020
QY 1071 CCGAGGGGATATACGGTCTTCATCTTCTGCGATGCGGAAGAGGCCACAAATGATACTA 1130
DB 1021 CCGAGGGGATATACGGTCTTCATCTTCTGCGATGCGGAAGAGGCCACAAATGATACTA 1080
QY 1131 TCTCTATTGGAAAAAGGTGCAAGTCATCAGAAGCACTTTTGGAGGTAGAACCGCACTC 1190
DB 1081 TCTCTATTGGAAAAAGGTGCAAGTCATCAGAAGCACTTTTGGAGGTAGAACCGCACTC 1140
QY 1191 ATGATCGCAAAAAAGCCACTATGCGGTTTGAATGTAATTAATATCCCGGAGCAATCAAG 1250
DB 1141 ATGATCGCAAAAAAGCCACTATGCGGTTTGAATGTAATTAATATCCCGGAGCAATCAAG 1200
QY 1251 CATTTCTCTCAAGGCCGACTATGCTAGAAATCTAGAGCAAGAGACAAACAGAGACAA 1310
DB 1201 CATTTCTCTCAAGGCCGACTATGCTAGAAATCTAGAGCAAGAGACAAACAGAGACAA 1260
QY 1311 ATTTCTAGAGATGTTCTCCCTCTTTTTCAGTGGCGGCGGATGAATTTGAAGATGACGCTG 1370
DB 1261 ATTTCTAGAGATGTTCTCCCTCTTTTTCAGTGGCGGCGGATGAATTTGAAGATGACGCTG 1320
QY 1371 CTCGATCTTTGAAATAGAGTTGCACTTGTCAACGCTCTTTTTCACGGAAGACACAGCT 1430
DB 1321 CTCGATCTTTGAAATAGAGTTGCACTTGTCAACGCTCTTTTTCACGGAAGACACAGCT 1380
QY 1431 GCAATGGAGATCGCGAAATGAAGGAACTGTGAGTTTCATAGTACGTAGCTCGAGGCT 1490
DB 1381 GCAATGGAGATCGCGAAATGAAGGAACTGTGAGTTTCATAGTACGTAGCTCGAGGCT 1440
QY 1491 GACCGTCTCACTGGTACGAGAGACATCACCAGGTGTAAAGATAGACCTTTTCAGAAATC 1550
DB 1441 GACCGTCTCACTGGTACGAGAGACATCACCAGGTGTAAAGATAGACCTTTTCAGAAATC 1500
QY 1551 CTAGAAGACATCAAGTAGACTAAAAGCGCTTTCTTAAACCGGTGGAAGTCCGGAACGA 1610
DB 1501 CTAGAAGACATCAAGTAGACTAAAAGCGCTTTCTTAAACCGGTGGAAGTCCGGAACGA 1560
QY 1611 TTCTTCCCGCGGTGTTTCGGCAGTGTCTGACACGATTTATGAATGT 1655
DB 1561 TTCTTCCCGCGGTGTTTCGGCAGTGTCTGACACGATTTATGAATGT 1605
|||||

Db 1202 CTCAACTGGCTTCGGGAGAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGT 1261
Qy 1726 ACATGGAATACAGAGACACTAAAGAGCCCTTTAGTGAGGACAATTTGGAAATTAGGAA 1785
Db 1262 ACATGGAATACAGAGACACTAAAGAGCCCTTTAGTGAGGACAATTTGGAAATTAGGAA 1321
Qy 1786 ATTGCGCCCTGACAGATTGCACTTCCTCCACATCGAAATCAACCGGTGCAAGAGGTCTA 1845
Db 1322 ATTGCGCCCTGACAGATTGCACTTCCTCCACATCGAAATCAACCGGTGCAAGAGGTCTA 1381
Qy 1846 ACCGTAACCTCTCATCGCTGCGGTGAGACTCTTGCCTCTTAGTGTAATTTTGCCTG 1905
Db 1382 ACCGTAACCTCTCATCGCTGCGGTGAGACTCTTGCCTCTTAGTGTAATTTTGCCTG 1441
Qy 1906 ACCATATAATTCGTTTTCATGACTGTAAGTCTTATGCTATGCTGCGTCATAT 1965
Db 1442 ACCATATAATTCGTTTTCATGACTGTAAGTCTTATGCTATGCTGCGTCATAT 1501
Qy 1966 AGTTTCGCTCTCGTTTTCATGCTGCTGATTAATTCGTCAGGTGCTTCAACAAATG 2025
Db 1502 AGTTTCGCTCTCGTTTTCATGCTGCTGATTAATTCGTCAGGTGCTTCAACAAATG 1561
Qy 2026 TTGTAACAAATTTGAACCAATGGTATACAGATTGTA 2061
Db 1562 TTGTAACAAATTTGAACCAATGGTATACAGATTGTA 1597

RESULT 15
AAV43662
ID AAV43662 standard; cDNA; 1597 BP.
AC AAV43662;
XX 29-SEP-1998 (first entry)
XX Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA.
KW Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;
KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;
KW constitutive immunity; agriculture; variant; ss.

XX Arabidopsis thaliana.
OS Synthetic.
XX Key Location/Qualifiers
FT CDS 1..1410
FT /*tag= a
FT /product= "NIM1 protein variant 2"
FT /note= "N-terminal deletion compared to wild-type
NIM1 sequence"

W09826082-A1.
XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-EP07012.
XX 20-JUN-1997; 97US-0880179.
PR 13-DEC-1996; 96US-0033177.
PR 27-DEC-1996; 96US-0034379.
PR 27-DEC-1996; 96US-0034382.
PR 10-JAN-1997; 97US-0034730.
PR 10-JAN-1997; 97US-0035021.
PR 10-JAN-1997; 97US-0035022.
XX (NOVS) NOVARTIS AG.
XX Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;
PI Uknes SJ;
XX WPI; 1998-348536/30.
DR P-PSDB; AAW61984.

XX Use of non-inducible immunity-1 gene - for transforming plants to
PT produce transgenic plants having a broad spectrum disease resistance
XX Claim 9; Pages 149-152; 205pp; English.
XX This cDNA encodes an altered form of the Arabidopsis thaliana non-
CC inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
CC AAV43665 represent variants of the NIM1 cDNA. The invention provides a
CC chimeric gene comprising a promoter active in plants operatively linked
CC to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
CC cells stably transformed with a recombinant vector comprising such a
CC chimeric gene have a broad spectrum of disease resistance. The altered
CC NIM1 proteins act as dominant-negative regulators of the systemic
CC acquired resistance (SAR) signal transduction pathway. The transgenic
CC plants transformed with an altered NIM1 gene exhibits constitutive SAR
CC expression which is higher in the transformed plants than in a wild-type
CC plant. The products can be used for producing plants with a broad
CC spectrum disease resistance. Overexpression of NIM1 mimics the effects
CC of inducer compounds that induce constitutive immunity (CIM) phenotype
CC in plants. The inventions can be used with plants such as rice, wheat,
CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
CC chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
CC tomato, sorghum and sugarcane. The plants produced are resistant to
CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such
CC as aphids and lepidoptera and nematodes. The plants produced can be used
CC in agriculture.
XX Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;
Qy Query Match 75.7%; Score 1592.8; DB 19; Length 1597;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 456 TCGATTTCGGTTGTGACTCTTTTGGCTTATGTTTACAGCAGAGTGTGAGCCGCGCTA 525
Db 2 TGGATTTCGGTTGTGACTCTTTTGGCTTATGTTTACAGCAGAGTGTGAGCCGCGCTA 61
Qy 526 AAGGAGTTTCTGAATGCGCAGCAGAGTGTGCTCCAGTGTGCTCCGCGCGCGGTGG 585
Db 62 AAGGAGTTTCTGAATGCGCAGCAGAGTGTGCTCCAGTGTGCTCCGCGCGCGGTGG 121
Qy 586 ATTTTCATGTTGAGGTTCTCTTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTA 645
Db 122 ATTTTCATGTTGAGGTTCTCTTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTA 181
Qy 646 TCTATCAGAGGCACTTATTTGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTA 705
Db 182 TCTATCAGAGGCACTTATTTGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTA 241
Qy 706 TACTCAAGCTTGCTAATATATGTTGTAAGCTTGTATGAAGCTATGATAGATGTAAG 765
Db 242 TACTCAAGCTTGCTAATATATGTTGTAAGCTTGTATGAAGCTATGATAGATGTAAG 301
Qy 766 AGATTATTGCAAGTCTAATGTAGATATGTTAGTCTTTGAAAAGTCAATTCGCGGAAGAGC 825
Db 302 AGATTATTGCAAGTCTAATGTAGATATGTTAGTCTTTGAAAAGTCAATTCGCGGAAGAGC 361
Qy 826 TTGTTAAAGAGATAATTGATAGAGCTAAAGAGCTTGGTTGGAGGTACCTAAAGTAAAGA 885
Db 362 TTGTTAAAGAGATAATTGATAGAGCTAAAGAGCTTGGTTGGAGGTACCTAAAGTAAAGA 421
Qy 886 AACATGCTCGAATGTACATAAGGCACCTTGACTCGAGTATGATGATGATGATGATGATG 945
Db 422 AACATGCTCGAATGTACATAAGGCACCTTGACTCGAGTATGATGATGATGATGATGATG 481
Qy 946 TTTTGAAGAGGATCACACCAATCTAGATGATGCTGTGCTCTTCAATTCGCTGCTTGCAT 1005
Db 482 TTTTGAAGAGGATCACACCAATCTAGATGATGCTGTGCTCTTCAATTCGCTGCTTGCAT 541

Search completed: October 7, 2002, 22:58:29
Job time : 321.819 secs

QY 1006 ATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTTGATCTTGCCGATGTCAACCATA 1065
DB 542 ATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTTGATCTTGCCGATGTCAACCATA 601
QY 1066 GGAATCCGAGGGGATATACGGTGTTCATGTGTGTCGATCGGAAGAGGCCAACATTGA 1125
DB 602 GGAATCCGAGGGGATATACGGTGTTCATGTGTGTCGATCGGAAGAGGCCAACATTGA 661
QY 1126 TACTATCTCTATTGAAAAGGTGCAAGTCATCAGAACAACTTTGGAAGGTAGAACC 1185
DB 662 TACTATCTCTATTGAAAAGGTGCAAGTCATCAGAACAACTTTGGAAGGTAGAACC 721
QY 1186 CACTCATGATCGCAAAAGCCACTATGCGGGTTGAATGTAATAATATCCCGGAGCAAT 1245
DB 722 CACTCATGATCGCAAAAGCCACTATGCGGGTTGAATGTAATAATATCCCGGAGCAAT 781
QY 1246 GCAAGCATTTCTCAAGGCCGACATGTGTAGAAATACTAGACAAAGAACAAAGAG 1305
DB 782 GCAAGCATTTCTCAAGGCCGACATGTGTAGAAATACTAGACAAAGAACAAAGAG 841
QY 1306 AACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAAGTGGCGCCGATGAATTGAGATGA 1365
DB 842 AACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAAGTGGCGCCGATGAATTGAGATGA 901
QY 1366 CGCTGCTCGATCTTGAANAATAGAGTTGCACITTGCTCAACGCTTTTCCAAACGGGAAGCAC 1425
DB 902 CGCTGCTCGATCTTGAANAATAGAGTTGCACITTGCTCAACGCTTTTCCAAACGGGAAGCAC 961
QY 1426 AAGCTGCAATGAGATCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCCTCG 1485
DB 962 AAGCTGCAATGAGATCGCCGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCCTCG 1021
QY 1486 AGCCTGACCGTCTCACTGCTACGAGAGAACATCACCGGCTTAAAGATAGCACCCTTCA 1545
DB 1022 AGCCTGACCGTCTCACTGCTACGAGAGAACATCACCGGCTTAAAGATAGCACCCTTCA 1081
QY 1546 GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGAACCTCGGGA 1605
DB 1082 GAATCCTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTAAAACCGTGAACCTCGGGA 1141
QY 1606 AAGCATTTCTCCCGGCTGTTCGGCAGTGTGCGACAGATTATGAACCTGTGAGGACTTGA 1665
DB 1142 AAGCATTTCTTCGCGGCTGTTCGGCAGTGTGCGACAGATTATGAACCTGTGAGGACTTGA 1201
QY 1666 CTCACCTGGCTTTCGAGAGACGACACTGCTGAGAAAGACTACAAAGAGCAAAAGGT 1725
DB 1202 CTCACCTGGCTTTCGAGAGACGACACTGCTGAGAAAGACTACAAAGAGCAAAAGGT 1261
QY 1726 ACATGGAATACAAGAGACACTAAAAGAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAA 1785
DB 1262 ACATGGAATACAAGAGACACTAAAAGAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAA 1321
QY 1786 ATTGTCCTGTACAGATTGAGTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTA 1845
DB 1322 ATTTGTCCCTGTACAGATTGAGTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTA 1381
QY 1846 ACCGTAAACTCTCATGCTCGCTGAGACTCTTGCTCTTAGTGTAATTTTGTGCTGT 1905
DB 1382 ACCGTAAACTCTCATGCTCGCTGAGACTCTTGCTCTTAGTGTAATTTTGTGCTGT 1441
QY 1906 ACCATATAATTTCTGTTTTCATGATGACGTAACTGTTTATGTCTATCGTTGGCGTCATAT 1965
DB 1442 ACCATATAATTTCTGTTTTCATGATGACGTAACTGTTTATGTCTATCGTTGGCGTCATAT 1501
QY 1966 AGTTTCGCTCTCGTTTTCATGATGACGTAACTGTTTATGTCTATCGTTGGCGTCATAT 2025
DB 1502 AGTTTCGCTCTCGTTTTCATGATGACGTAACTGTTTATGTCTATCGTTGGCGTCATAT 1561
QY 2026 TTGTAAACAATTTGAACCAATGGTATACAGATTTGTA 2061
DB 1562 TTGTAAACAATTTGAACCAATGGTATACAGATTTGTA 1597

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 22:39:34 ; Search time 45.7605 Seconds
(without alignments)
11293.859 Million cell updates/sec

Title: US-08-908-884-2

Perfect score: 2104

Sequence: 1 TCGATCTTTAAACCAATCCA.....ATAAAAAAAAAAAAAAAA 2104

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCRU_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2009.4	95.5	2011	2	US-08-989-478-6
2	2009.4	95.5	2011	3	US-08-996-685-6
3	2006.2	95.4	2011	2	US-08-989-478-7
4	2006.2	95.4	2011	3	US-08-996-685-7
5	1760	83.7	5655	2	US-08-989-478-1
6	1760	83.7	5655	3	US-08-996-685-1
7	1760	83.7	5655	3	US-08-980-179-2
8	1760	83.7	9919	3	US-08-880-179-1
9	1605	76.3	1608	2	US-08-989-478-11
10	1605	76.3	1608	3	US-08-996-685-11
11	1592.8	75.7	1597	2	US-08-989-478-9
12	1592.8	75.7	1597	3	US-08-996-685-9
13	1188.4	56.5	1194	2	US-08-989-478-13
14	1188.4	56.5	1194	3	US-08-996-685-13
15	781.4	37.1	786	2	US-08-989-478-15
16	781.4	37.1	786	3	US-08-996-685-15
17	49.6	2.4	7218	1	US-08-232-463-14
18	41.8	2.0	2296	4	US-08-496-841C-137
19	40.8	1.9	5852	1	US-07-867-106-2
20	39.6	1.9	2636	4	US-09-370-807-5
21	39	1.9	570	1	US-07-885-970A-10
22	39	1.9	570	1	US-08-298-687A-10
23	39	1.9	570	1	US-08-298-829-10
24	39	1.9	609	1	US-08-530-797-9
25	39	1.9	609	2	US-08-787-335-9
26	38.8	1.8	7218	1	US-08-232-463-14
27	37.2	1.8	1582	3	US-08-545-196B-10

28	37.2	1.8	1582	3	US-08-545-196B-12
29	36.8	1.7	436	4	US-09-439-313-353
30	36.6	1.7	789	6	5219739-8
31	36.6	1.7	3434	4	US-09-439-313-476
32	36.4	1.7	731	1	US-08-451-405A-2
33	36.4	1.7	790	6	5194596-8
34	36.4	1.7	961	6	5194596-16
35	36.4	1.7	961	6	5219739-16
36	36	1.7	374	4	US-09-385-982-494
37	35.8	1.7	567	4	US-09-385-982-427
38	35.4	1.7	8789	1	US-08-328-254-5
39	35.4	1.7	10136	1	US-08-353-700-2
40	35.4	1.7	10136	5	PCT-US95-16216-2
41	35.2	1.7	500	3	US-09-141-000-2
42	35	1.7	1908	2	US-08-909-965C-17
43	35	1.7	8220	2	US-08-568-459A-11
44	35	1.7	8220	2	US-08-487-826B-11
45	35	1.7	19124	2	US-08-487-826B-13

ALIGNMENTS

RESULT 1
US-08-989-478-6
; Sequence 6, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE N1M1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 2011 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..2011

OTHER INFORMATION: /note= "NIM1 cDNA sequence"

NAME/KEY: CDS

LOCATION: 43..1824

OTHER INFORMATION: /product= "NIM1 protein"

US-08-989-478-6

Query Match 95.5%; Score 2009.4; DB 2; Length 2011;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 51 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCAACCATTTGAT 110
DB 1 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCAACCATTTGAT 60

QY 111 GGATTCGCCGATCTTATGTAATATCAGCAGCACTAGTTTCGTGCTACCGGATTAACACCGAC 170
DB 61 GGATTCGCCGATCTTATGTAATATCAGCAGCACTAGTTTCGTGCTACCGGATTAACACCGAC 120

QY 171 TCCTCTATTTGTTATCTGCGCGCGGACAAAGTACTCACCGGACCTGATGTATCTGCTCTG 230
DB 121 TCCTCTATTTGTTATCTGCGCGCGGACAAAGTACTCACCGGACCTGATGTATCTGCTCTG 180

QY 231 CAATTGCTCTCCAAACAGCTTCGAATCCGCTTTGACTCGCGCGGATGATTTCTACACCGAC 290
DB 181 CAATTGCTCTCCAAACAGCTTCGAATCCGCTTTGACTCGCGCGGATGATTTCTACACCGAC 240

QY 291 GCTAAGCTTGTTCTCTCCGACGCGCGGGAAGTTTCTTTCCACCGTGCGTTTGTCCAGCG 350
DB 241 GCTAAGCTTGTTCTCTCCGACGCGCGGGAAGTTTCTTTCCACCGTGCGTTTGTCCAGCG 300

QY 351 AGAAGCTCTTCTTCAAGACGCTTTAGCGCGCGCTTAAGACGAGAAAGACTCCAAACAC 410
DB 301 AGAAGCTCTTCTTCAAGACGCTTTAGCGCGCGCTTAAGACGAGAAAGACTCCAAACAC 360

QY 411 ACCCGCGCGCTGAAGCTTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGGTTTCGAT 470
DB 361 ACCCGCGCGCTGAAGCTTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGGTTTCGAT 420

QY 471 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAGGA 530
DB 421 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTTAAGGA 480

QY 531 GTTTCTCAATTCGCGCAGACGAGAAATGCTGCCACGTGGCTTTCGCGCGCGCGGTGGATTTC 590
DB 481 GTTTCTCAATTCGCGCAGACGAGAAATGCTGCCACGTGGCTTTCGCGCGCGCGGTGGATTTC 540

QY 591 ATGTTGGAGGTTCTCTATTTGGCTTTCACTTCAAGATCCCTCAATTAATTAATCTCTAT 650
DB 541 ATGTTGGAGGTTCTCTATTTGGCTTTCACTTCAAGATCCCTCAATTAATTAATCTCTAT 600

QY 651 CAGAGGCACATTATGGACGTTGTAGACAAAGTTGTTATAGAGACACATTGGTTTATCTC 710
DB 601 CAGAGGCACATTATGGACGTTGTAGACAAAGTTGTTATAGAGACACATTGGTTTATCTC 660

QY 711 AAGCTTCTTAATATCTGCTGAAGCTTTGATGAAGCTATTGGATAGATGATAAAGAGATT 770
DB 661 AAGCTTCTTAATATCTGCTGAAGCTTTGATGAAGCTATTGGATAGATGATAAAGAGATT 720
```

QY 1851 AACTCTCTCATCGTCGTCGGTGAGACTCTTGCCCTCTTAGTGAATTTTGTCTGACCAT 1910
Db 1801 AACTCTCTCATCGTCGTCGGTGAGACTCTTGCCCTCTTAGTGAATTTTGTCTGACCAT 1860
QY 1911 ATAATCTGTTTTCATGATGACTGTAACGTGTTATGCTATCGTTGGCGTCATATAGTTT 1970
Db 1861 ATAATCTGTTTTCATGATGACTGTAACGTGTTATGCTATCGTTGGCGTCATATAGTTT 1920
QY 1971 CGCTCTCTGTTTTCATGATGACTGTTATGCTATCGTTGGCGTCATATAGTTT 2030
Db 1921 CGCTCTCTGTTTTCATGATGACTGTTATGCTATCGTTGGCGTCATATAGTTT 1980
QY 2031 ACAATTTGAACCAATGGTATACAGATTGTA 2061
Db 1981 ACAATTTGAACCAATGGTATACAGATTGTA 2011

RESULT 2
US-08-996-685-6
; Sequence 6, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Rvals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Ruess, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/PI/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2011
; OTHER INFORMATION: /note= "NIM1 cDNA sequence"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1824
; OTHER INFORMATION: /product= "NIM1 protein"
; US-08-996-685-6

Query Match 95.5%; Score 2009.4; DB 3; Length 2011;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 51 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACTTATGAT 110
Db 1 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACTTATGAT 60
QY 111 GGATTCGCCGATCTTATGAATCAGCAGACTAGTTTCGTCGCTACCGATACACCGAC 170
Db 61 GGATTCGCCGATCTTATGAATCAGCAGACTAGTTTCGTCGCTACCGATACACCGAC 120
QY 171 TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTACCGGACCTGATGTATCTGCTCTG 230
Db 121 TCCTCTATTGTTTATCTGGCCGCCGAACAAGTACTACCGGACCTGATGTATCTGCTCTG 180
QY 231 CAATTGCTCTCCAACAGCTTCGAATCCGTCCTTTGACTCGCCGGATGATTTCTACAGCGAC 290
Db 181 CAATTGCTCTCCAACAGCTTCGAATCCGTCCTTTGACTCGCCGGATGATTTCTACAGCGAC 240
QY 291 GCTAAGCTTTGTTCTCTCCGACGGCGGGAAGTTTCTTTCCACCGGTGGTTTTGTACGG 350
Db 241 GCTAAGCTTTGTTCTCTCCGACGGCGGGAAGTTTCTTTCCACCGGTGGTTTTGTACGG 300
QY 351 AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTTAAGAAGAGAAAGACTCCCAACAC 410
Db 301 AGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCCGCTTAAGAAGAGAAAGACTCCCAACAC 360
QY 411 ACCGCCGCGTGAAGCTGAGCTTAAGGAGATTGCAAGAGATTACGAAGTTCGTTTCGAT 470
Db 361 ACCGCCGCGTGAAGCTGAGCTTAAGGAGATTGCAAGAGATTACGAAGTTCGTTTCGAT 420
QY 471 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTACAGCCGCCGCTTAAGGA 530
Db 421 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTACAGCCGCCGCTTAAGGA 480
QY 531 GTTTCCTGAATGCGCAGACAGAAATTCGTCACAGTGGCTTCGCCGCCGCGGTGGATTTC 590
Db 481 GTTTCCTGAATGCGCAGACAGAAATTCGTCACAGTGGCTTCGCCGCCGCGGTGGATTTC 540
QY 591 ATGTTGGAGGTTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTAT 650
Db 541 ATGTTGGAGGTTCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTAT 600

QY 651 CAGAGGACTTATTGGAGCTTTAGACAAAGTTGTTATAGAGGACACATTGGTTATATCT 710
DB 601 CAGAGGACTTATTGGAGCTTTAGACAAAGTTGTTATAGAGGACACATTGGTTATATCT 660
QY 711 AAGCTTGCTAATATATATGTTAAAGCTTGTATGAAGCTTATTGGATAGATGTAAAGAGATT 770
DB 661 AAGCTTGCTAATATATATGTTAAAGCTTGTATGAAGCTTATTGGATAGATGTAAAGAGATT 720
QY 771 ATTGTCAAGTCTAATATAGATATGTTAGTCTTGAAGAGTCAATTCGCGGAAGAGCTTGT 830
DB 721 ATTGTCAAGTCTAATATAGATATGTTAGTCTTGAAGAGTCAATTCGCGGAAGAGCTTGT 780
QY 831 AAAGAGATAATTTGATAGACGTAAGAGCTTGTGAGAGTACCTTAAAGTAAAGAAACAT 890
DB 781 AAAGAGATAATTTGATAGACGTAAGAGCTTGTGAGAGTACCTTAAAGTAAAGAAACAT 840
QY 891 GTCTCGAATGTACATAAAGGCACTTGACCTCGGATGATATTGAGTTAGTCAAGTCTGTTTG 950
DB 841 GTCTCGAATGTACATAAAGGCACTTGACCTCGGATGATATTGAGTTAGTCAAGTCTGTTTG 900
QY 951 AAAGAGGATCACACCAATCTAGATGATGCTGCTCTTCAATTTGCGTGTTCGATATTGC 1010
DB 901 AAAGAGGATCACACCAATCTAGATGATGCTGCTCTTCAATTTGCGTGTTCGATATTGC 960
QY 1011 AATGTGAGACGCGCAACAGATCTTTTAAACCTTGATCTTGCAGTGTCAACCATAGGAAT 1070
DB 961 AATGTGAGACGCGCAACAGATCTTTTAAACCTTGATCTTGCAGTGTCAACCATAGGAAT 1020
QY 1071 CCGAGGGATATACGGTCTTCATCTTCTGCGATGCGGAAGGAGCCACAATTTGATACTA 1130
DB 1021 CCGAGGGATATACGGTCTTCATCTTCTGCGATGCGGAAGGAGCCACAATTTGATACTA 1080
QY 1131 TCTCTATTGGAAGAGGTCAGTGCATCAGAGCAACTTTGGAAGGTAGAACCCGACTC 1190
DB 1081 TCTCTATTGGAAGAGGTCAGTGCATCAGAGCAACTTTGGAAGGTAGAACCCGACTC 1140
QY 1191 ATGATCGCAAAACAGCCACTATGCGGTTGAATTAATAATATATATATATATATATATAT 1250
DB 1141 ATGATCGCAAAACAGCCACTATGCGGTTGAATTAATAATATATATATATATATATAT 1200
QY 1251 CATCTCTCAAGAGCGGACTATGTAGTAATACTAGAGCAAGAGACAAACGAGAAACA 1310
DB 1201 CATCTCTCAAGAGCGGACTATGTAGTAATACTAGAGCAAGAGACAAACGAGAAACA 1260
QY 1311 ATTCTTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGATGAATTTGAAGATGACGCTG 1370
DB 1261 ATTCTTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGATGAATTTGAAGATGACGCTG 1320
QY 1371 CTCGATCTTGAATAAGAGTTGCATTTGCTCAACGCTTTTTCACGGAAGCAAGCT 1430
DB 1321 CTCGATCTTGAATAAGAGTTGCATTTGCTCAACGCTTTTTCACGGAAGCAAGCT 1380
QY 1431 GCAATGGAGATGCCGAATGAAGGAACATCTGAGTTTCATAGTACCTAGCCTCGAGCT 1490
DB 1381 GCAATGGAGATGCCGAATGAAGGAACATCTGAGTTTCATAGTACCTAGCCTCGAGCT 1440
QY 1491 GACCGTCTCACTGTCAGGAAGAGAACATCACCGGCTGTTAAAGATAGCAGCTTTTCAAGATC 1550
DB 1441 GACCGTCTCACTGTCAGGAAGAGAACATCACCGGCTGTTAAAGATAGCAGCTTTTCAAGATC 1500
QY 1551 CTAGAAGAGATCAAAAGTATAGACTAAAGCGCTTTCTAAACCGTGAAGTCCGGGAACGA 1610
DB 1501 CTAGAAGAGATCAAAAGTATAGACTAAAGCGCTTTCTAAACCGTGAAGTCCGGGAACGA 1560
QY 1611 TTCTTCCGCGCTGTTCCGCGAGTCTGACGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 1670
DB 1561 TTCTTCCGCGCTGTTCCGCGAGTCTGACGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 1620
QY 1671 CTGGCTTGGGAGAGACGACACTGCTGAGAACGACTACAAAAGAGCAAAAGGTACATG 1730
DB 1621 CTGGCTTGGGAGAGACGACACTGCTGAGAACGACTACAAAAGAGCAAAAGGTACATG 1680
QY 1731 GAAATACAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAATTCG 1790

DB 1681 GAATACAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTTG 1740
QY 1791 TCCTTGACAGATTCGACTTCTTCCACATCGAATCAACCGGTGGAAGAGGCTTAACCGT 1850
DB 1741 TCCTTGACAGATTCGACTTCTTCCACATCGAATCAACCGGTGGAAGAGGCTTAACCGT 1800
QY 1851 AAACCTCTCATCGTCTGCGTGAGACTCTTGCTCTTAGTGTAAATTTTGTGCTGACCAT 1910
DB 1801 AAACCTCTCATCGTCTGCGTGAGACTCTTGCTCTTAGTGTAAATTTTGTGCTGACCAT 1860
QY 1911 ATAATCTGTTTTCATGATGACTGTAACTGTTTATGCTATATCGTTGGCCTCATATAGTTT 1970
DB 1861 ATAATCTGTTTTCATGATGACTGTAACTGTTTATGCTATATCGTTGGCCTCATATAGTTT 1920
QY 1971 CGCTCTCGTTTTGCACTCTGCTGATTAATGCTGCAAGTGTGCTTCAACAAATGTTGTA 2030
DB 1921 CGCTCTCGTTTTGCACTCTGCTGATTAATGCTGCAAGTGTGCTTCAACAAATGTTGTA 1980
QY 2031 ACAATTTGAACCAATGATACAGATTTGTA 2061
DB 1981 ACAATTTGAACCAATGATACAGATTTGTA 2011

RESULT 3
US-08-989-478-7
; Sequence 7, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2011 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 43..1824

OTHER INFORMATION: /product= "altered form of NIM1"

OTHER INFORMATION: /note= "Serine residues at amino acid positions 55 and 59 in

OTHER INFORMATION: wild-type NIM1 gene product have been changed to Alanine

OTHER INFORMATION: residues."

FEATURE:

NAME/KEY: misc_feature

LOCATION: 205..217

OTHER INFORMATION: /note= "nucleotides 205 and 217

OTHER INFORMATION: changed from T's to G's compared to wild-type sequence."

US-08-989-478-7

Query Match 95.4%; Score 2066.2; DB 2; Length 2011;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2008; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTGTGACACACCACTTGAT 110

DB 1 GATCTCTTTAATTTGTGAATTTCAATTCATCGGAACCTGTGTGACACACCACTTGAT 60

QY 111 GGATTCCGCGATTCCTTATGAATCAGCAGCACTAGTTTCGCTCCGCTACCGAATAACCCGAC 170

DB 61 GGATTCCGCGATTCCTTATGAATCAGCAGCACTAGTTTCGCTCCGCTACCGAATAACCCGAC 120

QY 171 TCCCTATTGTTTATCTGGCGCGGCGAACAAGTACTACCGGACCTGATGATCTGCTCTG 230

DB 121 TCCCTATTGTTTATCTGGCGCGGCGAACAAGTACTACCGGACCTGATGATCTGCTCTG 180

QY 231 CAATTGCTCTCAACAGCTTGAATTCGCTCTTTGACTCGCCGGATGATTTCTACACGCGAC 290

DB 181 CAATTGCTCTCAACAGCTTGAATTCGCTCTTTGACTCGCCGGATGATTTCTACACGCGAC 240

QY 291 GCTAAGCTTGTTCTCCGACGCGCGGGAAGTTCTTCCACCGGTCGCTTTGTCAGCG 350

DB 241 GCTAAGCTTGTTCTCCGACGCGCGGGAAGTTCTTCCACCGGTCGCTTTGTCAGCG 300

QY 351 AGAAGCTCTTTCTCAAGAGCGCTTTAGCCGCGCTTAAGAGGAGAAAGACTCCAACAAC 410

DB 301 AGAAGCTCTTTCTCAAGAGCGCTTTAGCCGCGCTTAAGAGGAGAAAGACTCCAACAAC 360

QY 411 ACCGCGCGCTGAAGCTCGAGCTTAAGAGATGCGCAAGGATTAAGAGTTCGAT 470

DB 361 ACCGCGCGCTGAAGCTCGAGCTTAAGAGATGCGCAAGGATTAAGAGTTCGAT 420

QY 471 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGTGTAGACCGCGCTTAAGGA 530

DB 421 TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGTGTAGACCGCGCTTAAGGA 480

QY 531 GTTTCGTAATCGGACGAGAAATGCTGCCAGTGCTGCGCGCGCGGCGGATTC 590

DB 481 GTTTCGTAATCGGACGAGAAATGCTGCCAGTGCTGCGCGCGCGGCGGATTC 540

QY 591 ATGTTGGAGGTTCTTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTAT 650

DB 541 ATGTTGGAGGTTCTTATTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTAT 600

QY 651 CAGAGGCACTTATTTGGAGCTTTGAGACAAAGTTGTTATAGAGGACACATTTGGTTACTC 710

DB 601 CAGAGGCACTTATTTGGAGCTTTGAGACAAAGTTGTTATAGAGGACACATTTGGTTACTC 660

QY 711 AAGCTTGCTAATATATGCTGTAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT 770

DB 661 AAGCTTGCTAATATATGCTGTAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATT 720

QY 771 ATTGTCAGTCTAATGTAGATATGGTTAGTCTTGAAGTCATTGCGGGAAGAGCTTTGTT 830

DB 721 ATTGTCAGTCTAATGTAGATATGGTTAGTCTTGAAGTCATTGCGGGAAGAGCTTTGTT 780

QY 831 AAAGAGATAATTGATAGACGTAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACAT 890

DB 781 AAAGAGATAATTGATAGACGTAAGAGCTTGGTTTGGAGTACCTAAAGTAAAGAAACAT 840

QY 891 GTCTCGAATGPACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950

DB 841 GTCTCGAATGPACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 900

QY 951 AAAGAGATCACCAATCTAGATGATGCGTCTCTTCATTTCCGCTGTTGCTATATTGC 1010

DB 901 AAAGAGATCACCAATCTAGATGATGCGTCTCTTCATTTCCGCTGTTGCTATATTGC 960

QY 1011 AATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGATGTCAACCATAGGAAT 1070

DB 961 AATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGATGTCAACCATAGGAAT 1020

QY 1071 CCGAGGGGATATACGGTCTTCATGTTGCTGCGATCGGAAGGAGCCACAAATGATACTA 1130

DB 1021 CCGAGGGGATATACGGTCTTCATGTTGCTGCGATCGGAAGGAGCCACAAATGATACTA 1080

QY 1131 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAACCACTTTGGAAGGTAGAACCGCACTC 1190

DB 1081 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAACCACTTTGGAAGGTAGAACCGCACTC 1140

QY 1191 ATGATCGCAAAACAAAGCCACTATGCGGTTGAATGTAAATATCCGAGCAATCGAAG 1250

DB 1141 ATGATCGCAAAACAAAGCCACTATGCGGTTGAATGTAAATATCCGAGCAATCGAAG 1200

QY 1251 CATCTCTCAAGGCCGACTATGTAGAAATCTACAGCAAGAACAAACAGAGAACAA 1310

DB 1201 CATCTCTCAAGGCCGACTATGTAGAAATCTACAGCAAGAACAAACAGAGAACAA 1260

QY 1311 ATTCTTAGAGATGTTCCCTCTTTTGCAGTGGCGCGGATGAATTTGAAGATGAGCGTG 1370

DB 1261 ATTCTTAGAGATGTTCCCTCTTTTGCAGTGGCGCGGATGAATTTGAAGATGAGCGTG 1320

QY 1371 CTCGATCTTGAATAAGATTGCACTTCTCAAGCTCTTTTCCACGGAAGCACAAGCT 1430

DB 1321 CTCGATCTTGAATAAGATTGCACTTCTCAAGCTCTTTTCCACGGAAGCACAAGCT 1380

QY 1431 GCAATGGAGATCGCCGAAATGAAGGAACTGTGAGTTCATAGTCTAGCCTCGAGCCT 1490

DB 1381 GCAATGGAGATCGCCGAAATGAAGGAACTGTGAGTTCATAGTCTAGCCTCGAGCCT 1440

QY 1491 GACCTCTCACTGTACGAGAGAACATCACCGGCTTAAGATAGCAGCTTTCAAGATC 1550

DB 1441 GACCTCTCACTGTGTACGAGAGAACATCACCGGCTTAAGATAGCAGCTTTCAAGATC 1500

QY 1551 CTAGAAGAGCATCAAAAGTAGACTTAAAGCGCTTTCTAAAAACCGTGGAACTCGGGAACGA 1610

DB 1501 CTAGAAGAGCATCAAAAGTAGACTTAAAGCGCTTTCTAAAAACCGTGGAACTCGGGAACGA 1560

QY 1611 TTCTTCCCGCCTGTTCGGCAGTCTCGACAGATTATGAATGTAGGAGCTTTGACTCAA 1670

DB 1561 TTCTTCCCGCCTGTTCGGCAGTCTCGACAGATTATGAATGTAGGAGCTTTGACTCAA 1620

QY 1671 CTGGCTTCGGGAGAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGATCATG 1730

DB 1621 CTGGCTTCGGGAGAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGATCATG 1680

QY 1731 GAATATCAAGAGACACTAAAGAACGCTTTAGTCAGGACAAATTTGGAATTAGGAAATTCG 1790

DB 1681 GAATATCAAGAGACACTAAAGAACGCTTTAGTCAGGACAAATTTGGAATTAGGAAATTCG 1740

QY 1791 TCCCTGACAGATTCGACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTTAACCGT 1850

QY 591 ATGTTGGAGGTTCTCTATTGGCTTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTCTAT 650
DB 541 ATGTTGGAGGTTCTCTATTGGCTTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTCTAT 600
QY 651 CAGAGGCATTTATTTGGAGGTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTATPACFC 710
DB 601 CAGAGGCATTTATTTGGAGGTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTATPACFC 660
QY 711 AAGCTTGTCTAATATATGTTGTAAGCTTTGATGAAGCTATTGGATAGATGTAAGAGATT 770
DB 661 AAGCTTGTCTAATATATGTTGTAAGCTTTGATGAAGCTATTGGATAGATGTAAGAGATT 720
QY 771 ATTGTCAAGTCTAATAGTAGATATGGTTAGTCTTTCAAAGTCATTTGCCGGAAGAGCTTTGT 830
DB 721 ATTGTCAAGTCTAATAGTAGATATGGTTAGTCTTTCAAAGTCATTTGCCGGAAGAGCTTTGT 780
QY 831 AAAGAGATAATTGATAGACGTAAGAGCTTTGGTTGGAGGTACCTAAAGTAAGAAACAT 890
DB 781 AAAGAGATAATTGATAGACGTAAGAGCTTTGGTTGGAGGTACCTAAAGTAAGAAACAT 840
QY 891 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 950
DB 841 GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 900
QY 951 AAAGAGGATCACCAATCTAGATGATGCGTGTGCTCTTCATTTCCGCTGTTGCATATTGC 1010
DB 901 AAAGAGGATCACCAATCTAGATGATGCGTGTGCTCTTCATTTCCGCTGTTGCATATTGC 960
QY 1011 AATGTGAAGACCGCAACAGATCTTTTAAACTTGCATCTCCGATGTCACACCATAGGAAT 1070
DB 961 AATGTGAAGACCGCAACAGATCTTTTAAACTTGCATCTCCGATGTCACACCATAGGAAT 1020
QY 1071 CCGAGGGGATATAGCGTCTTCATGTTGCTGCGATGCGGAAGGAGGCACAAATTTGATACTA 1130
DB 1021 CCGAGGGGATATAGCGTCTTCATGTTGCTGCGATGCGGAAGGAGGCACAAATTTGATACTA 1080
QY 1131 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC 1190
DB 1081 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTC 1140
QY 1191 ATGATCGCAAAACAGGCACATATGGCGTTGGAATTAATATCCGGAGCAATGCAAG 1250
DB 1141 ATGATCGCAAAACAGGCACATATGGCGTTGGAATTAATATCCGGAGCAATGCAAG 1200
QY 1251 CATCTCTCAAAAGCCGACTATGTTGTAGAAATCTAGAGCAAGAGCAACAGAGACAA 1310
DB 1201 CATCTCTCAAAAGCCGACTATGTTGTAGAAATCTAGAGCAAGAGCAACAGAGACAA 1260
QY 1311 ATTCCTAGAGATGTTCCCTCTCTTTTGCAGTGGCGGCGGATGAATTTGAAGATGACGCTG 1370
DB 1261 ATTCCTAGAGATGTTCCCTCTCTTTTGCAGTGGCGGCGGATGAATTTGAAGATGACGCTG 1320
QY 1371 CTCGATCTTGAATATAGAGTTGCACTTGTCTCAAGCTCTTTTCCAAAGGAGCACAAGCT 1430
DB 1321 CTCGATCTTGAATATAGAGTTGCACTTGTCTCAAGCTCTTTTCCAAAGGAGCACAAGCT 1380
QY 1431 GCAATGGAGATGCGGAAATGAAGGAACATGTTGAGTTTCAATGACTAGCTACGCTCGAGCCT 1490
DB 1381 GCAATGGAGATGCGGAAATGAAGGAACATGTTGAGTTTCAATGACTAGCTACGCTCGAGCCT 1440
QY 1491 GACCGTCTCACTGGTACCAGAGAACATCACCGGTTGTAAGATAGCACCTTTCAGAAATC 1550
DB 1441 GACCGTCTCACTGGTACCAGAGAACATCACCGGTTGTAAGATAGCACCTTTCAGAAATC 1500
QY 1551 CTAGAAGAGCATCAAGTAGACTAAAAGCGCTTTCTAAAACCGTTGGAACTCGGGAACGA 1610
DB 1501 CTAGAAGAGCATCAAGTAGACTAAAAGCGCTTTCTAAAACCGTTGGAACTCGGGAACGA 1560
QY 1611 TTCTTTCCGCGCTGTTCCGCGAGTCTCGACCAAGATTATGAACCTGTGAGGACTTGAACCAA 1670
DB 1561 TTCTTTCCGCGCTGTTCCGCGAGTCTCGACCAAGATTATGAACCTGTGAGGACTTGAACCAA 1620

RESULT 5

US-08-989-478-1

; Sequence 1, Application us/08989478

; Patent No. 5986082

; GENERAL INFORMATION:

; APPLICANT: Uknes, Scott

; APPLICANT: Hunt, Michelle

; APPLICANT: Steiner, Henry-York

; APPLICANT: Ryals, John

; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5986082artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: No. 5986082th Carolina

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,478

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/033,177

; FILING DATE: 13-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,379

; FILING DATE: 27-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,382

; FILING DATE: 27-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,730

; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,021

; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: MEIGS, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 2787..3347
OTHER INFORMATION: /product= "1st exon of NIM1"
FEATURE:
NAME/KEY: exon
LOCATION: 3427..4162
OTHER INFORMATION: /product= "2nd exon of NIM1"
FEATURE:
NAME/KEY: exon
LOCATION: 4271..4474
OTHER INFORMATION: /product= "3rd exon of NIM1"
FEATURE:
NAME/KEY: exon
LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
FEATURE:
NAME/KEY: CDS
LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-989-478-1

Query Match 83.7%; Score 1760; DB 2; Length 5655;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;

QY 1 TCGATCTTTAACCAATCCAGTTGATAGGTCCTTCGTTGATTAGCAGAGATCTCTTTA 60
DB 2695 TCGATCTTTAACCAATCCAGTTGATAGGTCCTTCGTTGATTAGCAGAGATCTCTTTA 2754
QY 61 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCAACCATTTGATTCGCCG 120
DB 2755 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCAACCATTTGATTCGCCG 2814
QY 121 ATTTCTATGAATCAGCAGCAGTCTAGTTTCGTCGCTACCGATACACCGACTCCTCTATTG 180
DB 2815 ATTTCTATGAATCAGCAGCAGTCTAGTTTCGTCGCTACCGATACACCGACTCCTCTATTG 2874
QY 181 TTTATCTGGCCGCCGCAACAAGTACTCACCGGACCTGATGATCTCTCTCTGCAATTTGCTCT 240
DB 2875 TTTATCTGGCCGCCGCAACAAGTACTCACCGGACCTGATGATCTCTCTCTGCAATTTGCTCT 2934
QY 241 CCAACAGCTTCGAATTCGCTCTTCTGACTCGCCGGATGATTTCTACAGCAGCCTAAAGCTTG 300
DB 2935 CCAACAGCTTCGAATTCGCTCTTCTGACTCGCCGGATGATTTCTACAGCAGCCTAAAGCTTG 2994
QY 301 TTTCTCTCGAGCGCCGGGAAGTTCTTTCCACCGGTGCGTTTGTCTACAGCAGGAAGCTCTT 360
DB 2995 TTTCTCTCGAGCGCCGGGAAGTTCTTTCCACCGGTGCGTTTGTCTACAGCAGGAAGCTCTT 3054
QY 361 TCTTCAAGAGCGCTTTAGCCCGCGGTGAAGAGGAGAAGACTCCAAACAACCCGCCGCCG 420
DB 3055 TCTTCAAGAGCGCTTTAGCCCGCGGTGAAGAGGAGAAGACTCCAAACAACCCGCCGCCG 3114
QY 421 TCAAGCTCGAGCTTAAGGAGATTGCGAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 480

DB 3115 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGA 3174
QY 481 CTGTTTTCGGCTTATGTTTACAGCAGCAGAGTGGAGCCGCCCTAAAGGAGTTTCTGAAT 540
DB 3175 CTGTTTTCGGCTTATGTTTACAGCAGCAGAGTGGAGCCGCCCTAAAGGAGTTTCTGAAT 3234
QY 541 GCGCAGACGAGAATTTGCTGCCACCTGGCTTCCCGCGCGCGGTGGATTTTCATGTTGGAG 600
DB 3235 GCGCAGACGAGAATTTGCTGCCACCTGGCTTCCCGCGCGCGGTGGATTTTCATGTTGGAG 3294
QY 601 TTCCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTCTA----- 649
DB 3295 TTCCTATTTGGCTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTCTATCAGGTAAC 3354
QY 650 ----- 649
DB 3355 ACCATCTGCATTAAAGCTATGTTTACACATTCATCAATATGTTCTTACTTGAGTACTTGA 3414
QY 650 -----TCAGAGCAGCTTATTTGGAGCTTGTAGACAAAGTTGTTATAGAGGACATTTG 701
DB 3415 TTTGTATTTTCAGAGCAGCTTATTTGGAGCTTGTAGACAAAGTTGTTATAGAGGACATTTG 3474
QY 702 GTTATACTCAAGCTTGTCTAATATATGTTGTAAGCTTGTATGAAGCTATTTGGATAGATGT 761
DB 3475 GTTATACTCAAGCTTGTCTAATATATGTTGTAAGCTTGTATGAAGCTATTTGGATAGATGT 3534
QY 762 AAAGAGATTATTGTCAAGTCTAATGTAGATATGTTAGTCTTGAAAAGTCATTTGCCGGA 821
DB 3535 AAAGAGATTATTGTCAAGTCTAATGTAGATATGTTAGTCTTGAAAAGTCATTTGCCGGA 3594
QY 822 GAGCTTGTAAAGAGATTAATGTAGACGCTAAGAGCTTGTGGAGGTACCTAAAGTA 881
DB 3595 GAGCTTGTAAAGAGATTAATGTAGACGCTAAGAGCTTGTGGAGGTACCTAAAGTA 3654
QY 882 AAGAAACATGTCTCGAATGTACATAAGCAGCTTGACCTCGGATGATTTGAGTTAGTCAAG 941
DB 3655 AAGAAACATGTCTCGAATGTACATAAGCAGCTTGACCTCGGATGATTTGAGTTAGTCAAG 3714
QY 942 TTGCTTTTGAAGAGGATCACCACCAATCTAGATGATCGGTGCTCTTCATTTTCGCTGTT 1001
DB 3715 TTGCTTTTGAAGAGGATCACCACCAATCTAGATGATCGGTGCTCTTCATTTTCGCTGTT 3774
QY 1002 GCATATTCGAATGTGAAGCCGCAACAGATCTTTTAAACCTTGATCTTGCCGATGTCAC 1061
DB 3775 GCATATTCGAATGTGAAGCCGCAACAGATCTTTTAAACCTTGATCTTGCCGATGTCAC 3834
QY 1062 CATAGGAATCCGAGGGATATACGGTGTCTCATGTTGCTCGGATGCGGAAGGACCAAA 1121
DB 3835 CATAGGAATCCGAGGGATATACGGTGTCTCATGTTGCTCGGATGCGGAAGGACCAAA 3894
QY 1122 TTGATACTATCTTATTTGGAAGAGGTGCAAGTGCATCAGAAGCAACTTTTGGAGGTAGA 1181
DB 3895 TTGATACTATCTTATTTGGAAGAGGTGCAAGTGCATCAGAAGCAACTTTTGGAGGTAGA 3954
QY 1182 ACCGCACTCATGATCGCAAAACAAGCCACTATGCGGTTTGAATGTATATATATCCCGGAG 1241
DB 3955 ACCGCACTCATGATCGCAAAACAAGCCACTATGCGGTTTGAATGTATATATATCCCGGAG 4014
QY 1242 CAATGCAAGCAATCTCTCAAGGCCGACTATGTAGAAAATCTAGAGCAAGAACAAA 1301
DB 4015 CAATGCAAGCAATCTCTCAAGGCCGACTATGTAGAAAATCTAGAGCAAGAACAAA 4074
QY 1302 CGAGAACAAATTCCTAGAGATGTTCCCTCCCTCTTTTTCAGTGGCGCGGATGAATGAAG 1361
DB 4075 CGAGAACAAATTCCTAGAGATGTTCCCTCCCTCTTTTTCAGTGGCGCGGATGAATGAAG 4134
QY 1362 ATGAGCTGCTCGATCTTGAATAAG----- 1387
DB 4135 ATGAGCTGCTCGATCTTGAATAAGATAGAGGTATCTATCAAGTCTTATTTCTTATATGTTG 4194
QY 1388 ----- 1387
DB 4195 AATTAAATTTATGCTCTCTCTATTAGGAAAGTGAAGTGAATGATGATGATGATTTCTTTG 4254


```
; NAME/KEY: exon
; LOCATION: 4586..4866
; OTHER INFORMATION: /product= "4th exon of NIM1"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
; US-08-996-685-1

Query Match      83.7%; Score 1760; DB 3; Length 5655;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;

QY 1 TCGATCTTTAAACCAATCCAGTGTGATAAGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60
Db 2695 TCGATCTTTAAACCAATCCAGTGTGATAAGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 2754

QY 61 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGACACACCACCATTTGATGGATTGCGCG 120
Db 2755 ATTTGTGAATTTCAATTCATCGGAACCTGTTGATGACACACCACCATTTGATGGATTGCGCG 2814

QY 121 ATTCCTTATGAATCAGCAGCAGTATGTTTCGTCGTACCGGATACACCGACTCTCTATTG 180
Db 2815 ATTCCTTATGAATCAGCAGCAGTATGTTTCGTCGTACCGGATACACCGACTCTCTATTG 2874

QY 181 TTTATCTGGCGCGCGAACAAGTACTACCGGAGCTGATGATCTGCTCTGCAATTGCTCT 240
Db 2875 TTTATCTGGCGCGCGAACAAGTACTACCGGAGCTGATGATCTGCTCTGCAATTGCTCT 2934

QY 241 CCAACAGCTTGAATCCGTCCTTTGACTGCGCGGATGATTTCTACAGCGAGGCTTAAGCTTG 300
Db 2935 CCAACAGCTTGAATCCGTCCTTTGACTGCGCGGATGATTTCTACAGCGAGGCTTAAGCTTG 2994

QY 301 TTTCTCTCGAGCGCGGGAAGTTTCTTTCCACCGGTGCGTTTGTGACGAGAGAAGTCTTT 360
Db 2995 TTTCTCTCGAGCGCGGGAAGTTTCTTTCCACCGGTGCGTTTGTGACGAGAGAAGTCTTT 3054

QY 361 TCTTCAAGAGCGCTTTAGCCGCGCTTAAGAGGAGAAGACTCCAACAACACCGCGCGCG 420
Db 3055 TCTTCAAGAGCGCTTTAGCCGCGCTTAAGAGGAGAAGACTCCAACAACACCGCGCGCG 3114

QY 421 TGAAGCTCGAGCTTTAAGGAGATGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTA 480
Db 3115 TGAAGCTCGAGCTTTAAGGAGATGCCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTA 3174

QY 481 CTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGAGATTTCTGAAT 540
Db 3175 CTGTTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCCTAAAGAGATTTCTGAAT 3234

QY 541 GCGCAGACGAGAAATTGCTGCCACGTGGCTTCCGCGCGCGCGGTGGATTTCAATGTTGAGG 600
Db 3235 GCGCAGACGAGAAATTGCTGCCACGTGGCTTCCGCGCGCGCGGTGGATTTCAATGTTGAGG 3294

QY 601 TTCCTATTTCGCTTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTA----- 649
Db 3295 TTCCTATTTCGCTTTTCATCTTCAAGATCCCTGAATTAATTAATCTCTAATCAGGTA AAC 3354

QY 650 ----- 649
Db 3355 ACCATCTGCAATTAAGCTATGGTTACACATTATGTTCTTACTTTCGATTCGTA 3414

QY 650 -----TCAGAGCGACTTATTGGAGCTGTGACAGAAAGTTGTTATAGAGGACACATTG 701
Db 3415 TTTGATTTTCAGAGCGACTTATTGGAGCTGTGACAGAAAGTTGTTATAGAGGACACATTG 3474

QY 702 GTTATCTCAAGCTTGCTTAATATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 761
Db 3475 GTTATCTCAAGCTTGCTTAATATATGTTGGTAAAGCTTGTATGAAGCTATTGGATAGATGT 3534

QY 762 AAAGAGATTATTGCAAGTCTTAATGATAGATAGTTAGTCTTGAAAAAGTCAATTCGCCGAA 821
Db 3535 AAAGAGATTATTGCAAGTCTTAATGATAGATAGTTAGTCTTGAAAAAGTCAATTCGCCGAA 3594

QY 822 GAGCTTGTAAAGAGATAATTGATAGAGCTTAAGAGCTTGGTTTGGAGGTACCTAAAGTA 881
```

```
Db 3595 GAGCTTGTAAAGAGATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTA 3654
QY 882 AAGAAACATGCTCGAATGTACATAAAGCACTTGACTCGGATGATATTGAGCTTAGTCAAG 941
Db 3655 AAGAAACATGCTCGAATGTACATAAAGCACTTGACTCGGATGATATTGAGCTTAGTCAAG 3714
QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGGTGTGCTCTTTCATTTCCGCTGTT 1001
Db 3715 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATGGTGTGCTCTTTCATTTCCGCTGTT 3774
QY 1002 GCATATTGCAATGTCAACCGCACAGATCTTTTAAACTTGATCTTTCGCGATGTCAC 1061
Db 3775 GCATATTGCAATGTCAACCGCACAGATCTTTTAAACTTGATCTTTCGCGATGTCAC 3834
QY 1062 CATAGGAATCCGAGGGATATACGGTGTCTCATGTGCTGCGATGCGGAAGAGCCACAA 1121
Db 3835 CATAGGAATCCGAGGGATATACGGTGTCTCATGTGCTGCGATGCGGAAGAGCCACAA 3894
QY 1122 TTGATACTATCTCTATTGGAAAAAGTGCAGTGCATCAGAAAGCACTTTTGAAGGTAGA 1181
Db 3895 TTGATACTATCTCTATTGGAAAAAGTGCAGTGCATCAGAAAGCACTTTTGAAGGTAGA 3954
QY 1182 ACCGCACTCATGATCGAAAAACAAGCCACTATGCGGTTGATGTAATAATATCCCGGAG 1241
Db 3955 ACCGCACTCATGATCGAAAAACAAGCCACTATGCGGTTGATGTAATAATATCCCGGAG 4014
QY 1242 CAATGCAAGCATTTCTCAAAGCGGAGCTATGTGTAGAAATACTAGAGCAAGAGACAAA 1301
Db 4015 CAATGCAAGCATTTCTCAAAGCGGAGCTATGTGTAGAAATACTAGAGCAAGAGACAAA 4074
QY 1302 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGGATGAATTGAAG 1361
Db 4075 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGGATGAATTGAAG 4134
QY 1362 ATGACGCTGCTCGATCTTGAAAAATAG----- 1387
Db 4135 ATGACGCTGCTCGATCTTGAAAAATAGAGGTATCTATCAAGTCTTATTTCTTATATGTTTG 4194
QY 1388 ----- 1387
Db 4195 AATTAAATTTATGCTCTCTATTAGGAACTGAGTGAACATAATGATAACTATTTCTTGT 4254
QY 1388 -----AGTTGCACCTTGCTCAACGCTCTTTTCCAAACGGAAGCACAAGCTGCA 1433
Db 4255 GTGCTCCACTGTTTGTGCTCAACGCTCTTTTCCAAACGGAAGCACAAGCTGCA 4314
QY 1434 ATGGAGATCGCGAAATGAAGGAAACATGTGAGTTCACTAGTCTCGAGCTGAC 1493
Db 4315 ATGGAGATCGCGAAATGAAGGAAACATGTGAGTTCACTAGTCTCGAGCTGAC 4374
QY 1494 CGTCTCACCTGGTACGAAGAGAACATCACCGGTTGTAAGATAGCACCTTTTCAGAATCCTA 1553
Db 4375 CGTCTCACCTGGTACGAAGAGAACATCACCGGTTGTAAGATAGCACCTTTTCAGAATCCTA 4434
QY 1554 GAAGAGCATCAAGTAGACTTAAAGCGCTTTCTAAACC----- 1592
Db 4435 GAAGAGCATCAAGTAGACTTAAAGCGCTTTCTAAACC----- 1592
QY 1593 ----- 1592
Db 4495 CATCGGACTCTTATTCACAAAAACAATAATGATCTTTAAACATGGTTTTTGTACT 4554
QY 1593 -----GTGGAACTCGGGAACAGATTCTTCCCGGCG 1622
Db 4555 TGCTGTCTGACCTGTTTTTTTATCATCAGTGAACCTCGGAAACGATTCTTCCCGGCG 4614
QY 1623 TGTTCGCGAGTGTCCAGCAGATTATGAAGTGTGAGGACTTCACTCAACTGCTTTCGCGA 1682
Db 4615 TGTTCGCGAGTGTCCAGCAGATTATGAAGTGTGAGGACTTCACTCAACTGCTTTCGCGA 4674
QY 1683 GAAGAGCAGACTGCTGAGAAAGAGCTTACAAAAAGAGCAAGGTACATGGAATACAAAG 1742
```

Db 4675 GAAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAAAGGTACATGTAATACAGAG 4734
QY 1743 ACACATAAAGAGGCTTTAGTAGGAGACAAATTTGGAATTAGAAATTCGTCCCTGACAGAT 1802
Db 4735 ACACATAAAGAGGCTTTAGTAGGAGACAAATTTGGAATTAGAAATTCGTCCCTGACAGAT 4794
QY 1803 TCGACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAACACTCTCTCAT 1862
Db 4795 TCGACTTCTTCCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAACACTCTCTCAT 4854
QY 1863 GTCGTCGGTGAGACTCTTGCGCTCTTAGTGTAAATTTTGTGTACCATATAAATTCCTGTTT 1922
Db 4855 GTCGTCGGTGAGACTCTTGCGCTCTTAGTGTAAATTTTGTGTACCATATAAATTCCTGTTT 4914
QY 1923 TCATGATGACTGTAACGTTTATCTCTATCTATCGTTGGCGTCATATAGTTTCGTCCTGTTT 1982
Db 4915 TCATGATGACTGTAACGTTTATCTCTATCTATCGTTGGCGTCATATAGTTTCGTCCTGTTT 4974
QY 1983 TGCATCCCTGTGTATTTATGCTGCAGGTGTGCTTCAAAACAAATGTTTAAACAAATTTGAACC 2042
Db 4975 TGCATCCCTGTGTATTTATGCTGCAGGTGTGCTTCAAAACAAATGTTTAAACAAATTTGAACC 5034
QY 2043 AATGGTATACAGATTTGTAATATATATATTTATGTACATCAACAATAA 2088
Db 5035 AATGGTATACAGATTTGTAATATATATATTTATGTACATCAACAATAA 5080

RESULT 7

US-08-880-179-2
; Sequence 2, Application US/08880179
; Patent No. 6091004
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Delaney, Terry
; APPLICANT: Friedrich, Leslie
; APPLICANT: Weymann, Kristianna
; APPLICANT: Lawton, Kay
; APPLICANT: Ellis, Daniel
; APPLICANT: Uknes, Scott
; APPLICANT: Jesse, Taco
; APPLICANT: Vos, Pieter
; TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE
; TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIS
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6091004artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,179
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1909
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2787..3347
; OTHER INFORMATION: /product= "1st exon of NIM1"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3427..4162
; OTHER INFORMATION: /product= "2nd exon of NIM1"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4271..4474
; OTHER INFORMATION: /product= "3rd exon of NIM1"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 4586..4866
; OTHER INFORMATION: /product= "4th exon of NIM1"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
; US-08-880-179-2

Query Match 83.7%; Score 1760; DB 3; Length 5655;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 298; Gaps 3;
QY 1 TCGATCTTTAACCAATCCAGTTGATAAGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 60
Db 2695 TCGATCTTTAACCAATCCAGTTGATAAGTCTCTTCGTTGATTAGCAGAGATCTCTTTA 2754
QY 61 ATTTGTGAATTTCAATTCATCGSAACCTGTTGATGACACACCACCAATGATGATTGCGCG 120
Db 2755 ATTTGTGAATTTCAATTCATCGSAACCTGTTGATGACACACCACCAATGATGATTGCGCG 2814
QY 121 ATTCCTTATGAATCAGCAGCAGTCTGTCGTCGCTACCGATTAACACCGACTCCTCTATTG 180
Db 2815 ATTCCTTATGAATCAGCAGCAGTCTGTCGTCGCTACCGATTAACACCGACTCCTCTATTG 2874
QY 181 TTATCTGCGCGCGCAACAAAGTACTCACCGGACCTGATGATCTCTGCAATTCCTCT 240
Db 2875 TTATCTGCGCGCGCAACAAAGTACTCACCGGACCTGATGATCTCTGCAATTCCTCT 2934
QY 241 CCAACAGCTTCGAATCCGTCCTTTGACTCCCGGATGATTTCTACAGCGACGCTAAGCTTG 300
Db 2935 CCAACAGCTTCGAATCCGTCCTTTGACTCCCGGATGATTTCTACAGCGACGCTAAGCTTG 2994
QY 301 TTCTCTCCGACGCGCGGGAAGTTTCTTCCACCGGTGCGTTTGTTCAGGAGAACTCTT 360
Db 2995 TTCTCTCCGACGCGCGGGAAGTTTCTTCCACCGGTGCGTTTGTTCAGGAGAACTCTT 3054
QY 361 TCTTCAAGAGCGCTTTAGCGCGCGCTAAGAAGGAGAAAGACTCCAAACACACCGCGCG 420
Db 3055 TCTTCAAGAGCGCTTTAGCGCGCGCTAAGAAGGAGAAAGACTCCAAACACACCGCGCG 3114
QY 421 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGGTTTCGATTGTTGA 480
Db 3115 TGAAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGGTTTCGATTGTTGA 3174
QY 481 CHTGTTTGGCTTATGTTTACAGCAGCAGAGTAGAGCCGCGCTAAAGAGTTTCTGAAT 540
Db 3175 CHTGTTTGGCTTATGTTTACAGCAGCAGAGTAGAGCCGCGCTAAAGAGTTTCTGAAT 3234
QY 541 GCGCAGACGAGAAATGCTGCCACGTGGCTTCCGCGCGCGGTGATTCATGTTGGAGG 600
Db 3235 GCGCAGACGAGAAATGCTGCCACGTGGCTTCCGCGCGCGGTGATTCATGTTGGAGG 3294
QY 601 TTCTCTATTGGCTTTCATCTTCAAGATCCCTGAAATTAATTAATTAATTAATTAATTAAT 649
Db 3295 TTCTCTATTGGCTTTCATCTTCAAGATCCCTGAAATTAATTAATTAATTAATTAATTAAT 3354

QY 650 ----- 649
Db 3355 ACCATCTGCATTAGCTATGGTTACACATTCATGAATATATCTTACTTGAGTACTTGTA 3414
QY 650 -----TCAGAGGCACCTTATTTGGAGCTTGTAGACAAAGTTGTTATAGAGGACACATTG 701
Db 3415 TTTGCTATTTAGAGGCACCTTATTTGGAGCTTGTAGACAAAGTTGTTATAGAGGACACATTG 3474
QY 702 GTTATATCAAGCTTGCTAATATATATGTTGAAAGCTGTATGAAGCTATTTGGATAGATGT 761
Db 3475 GTTATATCAAGCTTGCTAATATATATGTTGAAAGCTTGTATGAAGCTATTTGGATAGATGT 3534
QY 762 AAAGAGATTAATTGTCGAAGTCTAATGTAGATATGTTAGTCTTGAAAGAGTCATTGCCGGAA 821
Db 3535 AAAGAGATTAATTGTCGAAGTCTAATGTAGATATGTTAGTCTTGAAAGAGTCATTGCCGGAA 3594
QY 822 GAGCTTGTAAAGAGATTAATTGTATAGACGTAAAGAGCTTGTTGGAGGTACCTAAAGTA 881
Db 3595 GAGCTTGTAAAGAGATTAATTGTATAGACGTAAAGAGCTTGTTGGAGGTACCTAAAGTA 3654
QY 882 AAGAAACATGCTCGAATGTACATAAGGCACCTTGACCTCGATGATATTTAGTTAGTCAAG 941
Db 3655 AAGAAACATGCTCGAATGTACATAAGGCACCTTGACCTCGATGATATTTAGTTAGTCAAG 3714
QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGTGTGCTCTTCAATTTTCGCTGTT 1001
Db 3715 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGTGTGCTCTTCAATTTTCGCTGTT 3774
QY 1002 GCATATTGCAATGTGAAGCGGCAACAGATCTTTTAAACTTGTATTTGCCGATGTCAAC 1061
Db 3775 GCATATTGCAATGTGAAGCGGCAACAGATCTTTTAAACTTGTATTTGCCGATGTCAAC 3834
QY 1062 CATAGGAATCGAGGGGATATACGCTGCTCATGCTGCGATCGGAGGAGGAGCCACAA 1121
Db 3835 CATAGGAATCGAGGGGATATACGCTGCTCATGCTGCGATCGGAGGAGGAGCCACAA 3894
QY 1122 TTGATACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCACTTTGGAAGGTAGA 1181
Db 3895 TTGATACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCACTTTGGAAGGTAGA 3954
QY 1182 ACCGACCTCATGATCGCAAAACAGCCACTATGCGGTGGAATGTAATATATCCCGGAG 1241
Db 3955 ACCGACCTCATGATCGCAAAACAGCCACTATGCGGTGGAATGTAATATATCCCGGAG 4014
QY 1242 CAATGCAAGCATCTCTCAAAAGCGGCACTATGTTAGAAAATCTAGAGCAAGAGACAAA 1301
Db 4015 CAATGCAAGCATCTCTCAAAAGCGGCACTATGTTAGAAAATCTAGAGCAAGAGACAAA 4074
QY 1302 CGAGAACAAATTCCTAGAGATGTTCCCTCCCTCTTTTGCAGTGGCGGCGGATGAATGAAG 1361
Db 4075 CGAGAACAAATTCCTAGAGATGTTCCCTCCCTCTTTTGCAGTGGCGGCGGATGAATGAAG 4134
QY 1362 ATGAGCGTCTCGATCTTTGAAAATAG----- 1387
Db 4135 ATGAGCGTCTCGATCTTTGAAAATAGAGGTATCTCAAGTCTTATTTCTTATATGTTG 4194
QY 1388 ----- 1387
Db 4195 AATTAATTTATGCTCTCTATTAGGAAACTGAGTGAACCTAATGATAACTATTCTTTGT 4254
QY 1388 -----AGTTGCACCTTGCTCAACGCTCTTTTCCAAGCGGAGCACAGCTGCA 1433
Db 4255 GTGCTCCACTGTTTAGTTGCACTTGCTCAACGCTCTTTTCCAAGCGGAGCACAGCTGCA 4314
QY 1434 ATGAGATCGCGGAAATGAAGGGAACATGTGAGTTCATAGTACTAGCTCGAGCCTGAC 1493
Db 4315 ATGAGATCGCGGAAATGAAGGGAACATGTGAGTTCATAGTACTAGCTCGAGCCTGAC 4374
QY 1494 CGTCTACTGTTAGAGAGAACATCACCGGGTGTAAAGATPAGCACCTTTTCAGAACTCTTA 1553
Db 4375 CGTCTACTGTTAGAGAGAACATCACCGGGTGTAAAGATPAGCACCTTTTCAGAACTCTTA 4434
QY 1554 GAAGAGCATCAAGTAGACTAAAGCGGCTTTCTAAACCC----- 1592

Db 4435 GAAGAGCATCAAAAGTAGACTAAAGCGCTTCTTAAACCGGTATGGATTCTCACCCACTT 4494
QY 1593 ----- 1592
Db 4495 CATCGGACTCCTTATCACAAAAACAAACTAAATGATCTTTTAAACATGGTTTGTACT 4554
QY 1593 -----GTGGAACTCGGGAAACAGATTTCTCCCGGC 1622
Db 4555 TCCTGTCTGACCTTCTTTTATCATCAGTGGAACTCGGAAACAGATTTCTCCCGGC 4614
QY 1623 TGTTCGGAGTCTCGACAGATTAATGAACCTGTGAGGACTTGACTCAACTGCTTGC CGGA 1682
Db 4615 TGTTCGGAGTCTCGACAGATTAATGAACCTGTGAGGACTTGACTCAACTGCTTGC CGGA 4674
QY 1683 GAAGAGCACCTCTGAGAAACGACTACAAAAGAGCAAGGTACATGGAATACAAGAG 1742
Db 4675 GAAGAGCACCTGCTGAGAAACGACTACAAAAGAGCAAGGTACATGGAATACAAGAG 4734
QY 1743 ACACATAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTCGCTCGACAGAT 1802
Db 4735 ACACATAAGAGGCGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTCGCTCGACAGAT 4794
QY 1803 TCGACTTCTTCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT 1862
Db 4795 TCGACTTCTTCACATCGAAATCAACCGGTGGAAGAGGTCTAACCGTAAACTCTCTCAT 4854
QY 1863 CGTCGTCGTGAGACTCTTTCGCTCTTAGTGTAAATTTTGTGTACCATATAATTTCTGTTT 1922
Db 4855 CGTCGTCGTGAGACTCTTTCGCTCTTAGTGTAAATTTTGTGTACCATATAATTTCTGTTT 4914
QY 1923 TCATGATGACTGTAACCTGTTTATGCTATGCTGTCGTCATATAGTTTCGCTCTTCGTTT 1982
Db 4915 TCATGATGACTGTAACCTGTTTATGCTATGCTGTCGTCATATAGTTTCGCTCTTCGTTT 4974
QY 1983 TGCATCCTCTGTATTTATGCTCAGGTGCTTCAACAAATTTGTAACAAATTTGAACC 2042
Db 4975 TGCATCCTCTGTATTTATGCTCAGGTGCTTCAACAAATTTGTAACAAATTTGAACC 5034
QY 2043 AATGTTATACAGATTTGTAATATATATATATTTATGATACATCAACAATAA 2088
Db 5035 AATGTTATACAGATTTGTAATATATATATATTTATGATACATCAACAATAA 5080

RESULT 8

US-08-880-179-1/c

; Sequence 1, Application US/08880179

; Patent No. 6091004

; GENERAL INFORMATION:

; APPLICANT: Ryals, John

; APPLICANT: Delaney, Terry

; APPLICANT: Friedrich, Leslie

; APPLICANT: Weymann, Kristianna

; APPLICANT: Lawton, Kay

; APPLICANT: Ellis, Daniel

; APPLICANT: Uknes, Scott

; APPLICANT: Jesse, Peter

; APPLICANT: Vos, Dieter

; TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE

; TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RE

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6091004artis Corporation

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: USA

; ZIP: 10591

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,179
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1909
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9919 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-880-179-1

Query Match      83.7%  Score 1760;  DB 3;  Length 9919;
Best Local Similarity 87.5%;  Pred.No 0;
Matches 2088;  Conservative 0;  Mismatches 0;  Indels 298;  Gaps 3;

QY 1 TCGATCTTTAACCAAAATCCAGTTCATAGAGTCTCTTCGTTGATAGCAGAGATCTCTTTA 60
DB TCGATCTTTAACCAAAATCCAGTTCATAGAGTCTCTTCGTTGATAGCAGAGATCTCTTTA 3808

QY 61 ATTTGTGAATTTCAATTCATCGGAACCTGTGATGGACACACCATGTGATTCGCCG 120
DB ATTTGTGAATTTCAATTCATCGGAACCTGTGATGGACACACCATGTGATTCGCCG 3748

QY 121 ATTTCTATGAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCTCTATTG 180
DB ATTTCTATGAATCAGCAGCACTAGTTTCGTCGCTACCGATAACACCGACTCTCTATTG 3688

QY 181 TTATCTGGCGCGGCAACAGTACTACCGGACCTGATGATCTGCTGCTGCAATTCCT 240
DB TTATCTGGCGCGGCAACAGTACTACCGGACCTGATGATCTGCTGCTGCAATTCCT 3628

QY 241 CCAACAGCTTCGAATCCGCTTTGACTCGCGGATGATTTCTACAGCGACGCTAAGCTTG 300
DB CCAACAGCTTCGAATCCGCTTTGACTCGCGGATGATTTCTACAGCGACGCTAAGCTTG 3568

QY 301 TTCTCTCGAGCGCGGGAAGTTTCTTTCACCGGTCGTTTGTTCAGCGAGAGCTCTT 350
DB TTCTCTCGAGCGCGGGAAGTTTCTTTCACCGGTCGTTTGTTCAGCGAGAGCTCTT 3508

QY 361 TCTTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCTCAACACACCGCGCGCG 420
DB TCTTCAAGAGCGCTTTAGCCGCGCTAAGAGGAGAAAGACTCTCAACACACCGCGCGCG 3448

QY 421 TGAAGCTCAGCTTAAGAGATATGCCAAGGATACGAAGTCGGTTTCGATTCGGTTGTGA 480
DB TGAAGCTCAGCTTAAGAGATATGCCAAGGATACGAAGTCGGTTTCGATTCGGTTGTGA 3388

QY 481 CTGTTTTCGGCTTATGTTTACAGCAGCAGAGTACAGCGCGCTTAAAGAGGATTTCTGAAT 540
DB CTGTTTTCGGCTTATGTTTACAGCAGCAGAGTACAGCGCGCTTAAAGAGGATTTCTGAAT 3328

QY 541 GCGCAGACGAGAAATTCGTCACGCTGGGTTGCCGCGCGCGGTTGATTTTCATGTTGGAGG 600
DB GCGCAGACGAGAAATTCGTCACGCTGGGTTGCCGCGCGCGGTTGATTTTCATGTTGGAGG 3268

QY 601 TTCTCTATTTCGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTA 649
DB TTCTCTATTTCGCTTTCATCTTCAAGATCCCTGAATTAATTAATTAATTAATTAATTA 3208

QY 650 ----- 1592
DB ----- 2068
```

```

DB 3207 ACCATCTGCATTAAGCTATGGTTACACATTCATGAATATCTTCTTACTTGAGTACTGTA 3148
QY 650 -----TCAGAGGCACTTATTTGGACGTTGTAGACAAAGTCTTCTTATAGAGGACACATTG 701
DB 3147 TTTGTATTTTCAGAGGCACTTATTTGGACGTTGTAGACAAAGTCTTCTTATAGAGGACACATTG 3088
QY 702 GTTATCTCAAGCTTGCTAATATATATGTGTAAAGCTTTGTATGAAGCTATTGGATAGATCT 761
DB 3087 GTTATCTCAAGCTTGCTAATATATATGTGTAAAGCTTTGTATGAAGCTATTGGATAGATCT 3028
QY 762 AAAGAGATTTATGCAAGTCTAATGTAGATATGGTTAGTCTTCAAAAGTCAATTCGCGGAA 821
DB 3027 AAAGAGATTTATGCAAGTCTAATGTAGATATGGTTAGTCTTCAAAAGTCAATTCGCGGAA 2968
QY 822 CAGCTTCTTAAAGAGATAAATTCATAGACGTAAGAGAGCTTGGTTTGGAGGTACCTAAAGTA 881
DB 2967 CAGCTTCTTAAAGAGATAAATTCATAGACGTAAGAGAGCTTGGTTTGGAGGTACCTAAAGTA 2908
QY 882 AAGAAACATGCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGATTTAGTCAAG 941
DB 2907 AAGAAACATGCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGATTTAGTCAAG 2848
QY 942 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGTGTCTCTTCAATTTCCGCTGT 1001
DB 2847 TTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGTGTCTCTTCAATTTCCGCTGT 2788
QY 1002 GCATATTCGAATGTGAAGACGCGCAACAGATCTTTTAAACTTGATCTTGCCGATGTCAAC 1061
DB 2787 GCATATTCGAATGTGAAGACGCGCAACAGATCTTTTAAACTTGATCTTGCCGATGTCAAC 2728
QY 1062 CATAGGAATCGAGGATATACGCTGCTTCATGCTCGGATCGGAGGAGCCACAA 1121
DB 2727 CATAGGAATCGAGGATATACGCTGCTTCATGCTCGGATCGGAGGAGCCACAA 2668
QY 1122 TTGACTATCTCTATTGGAAGAGGTCGAAGTGCATCAGAAGCAACTTTTGAAGTAGA 1181
DB 2667 TTGACTATCTCTATTGGAAGAGGTCGAAGTGCATCAGAAGCAACTTTTGAAGTAGA 2608
QY 1182 ACCGCACTCATGTCGCAAAACAGCCACTATGCGGTTGAAATGTAATATATATATATATATAT 1241
DB 2607 ACCGCACTCATGTCGCAAAACAGCCACTATGCGGTTGAAATGTAATATATATATATATATAT 2548
QY 1242 CAATGCAAGCACTCTCTCAAGAGCCGACTATGTGTAGAAATAGTAGCAAGAGAGCAAA 1301
DB 2547 CAATGCAAGCACTCTCTCAAGAGCCGACTATGTGTAGAAATAGTAGCAAGAGAGCAAA 2488
QY 1302 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTCAGTGGCGCGGATGAATGAAG 1361
DB 2487 CGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTCAGTGGCGCGGATGAATGAAG 2428
QY 1362 ATGAGCTGCTCGATCTTTGAAATAG ----- 1387
DB 2427 ATGAGCTGCTCGATCTTTGAAATAGAGGTATCTATCAAGTCTTATTTCTTATATGTTG 2368
QY 1388 ----- 1387
DB 2367 AATTAAATTTATGCTCTCTCTATTAGGAAACTGAGTCAACTAATGATAACTATTCCTTGT 2308
QY 1388 -----AGTTGCACTTGCTCAACGCTCTTTTCCACGGAAGCAGCAAGCTGCA 1433
DB 2307 GTCGTCCTACTCTTTAGTTGCACTTGCTCAAGCTCTTTTCCACGGAAGCAGCAAGCTGCA 2248
QY 1434 ATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCGAGCCTGAC 1493
DB 2247 ATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCGAGCCTGAC 2188
QY 1494 GCTCTCACTGTTACGAAGAGAACATCACCGGTTGTAAGATAGCACCTTTTCAAGATCCCTA 1553
DB 2187 GCTCTCACTGTTACGAAGAGAACATCACCGGTTGTAAGATAGCACCTTTTCAAGATCCCTA 2128
QY 1554 GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTTAAACC ----- 1592
DB 2127 GAAGAGCATCAAAGTAGACTAAAAGCGCTTTCTTAAACC ----- 1592
```

QY 1593 ----- 1592
Db 2067 CATCGGACTCCTTTATCACAAACAAACAACTAAATGATCTTTAAACATGGTTTGTACT 2008
QY 1593 -----GTGGAAGTGGGAAAGGATTCCTCCGCGC 1622
Db 2007 TGCTGTCTGACCTGTGTTTTTATCATCAGTGGAACTCGGAAAGGATTCCTCCGCGC 1948
QY 1623 TGTTCGGCAGTGTCTGACAGATTAATGAATGTGAGGACTTGAATCACTGGCTTGCAGG 1682
Db 1947 TGTTCGGCAGTGTCTGACAGATTAATGAATGTGAGGACTTGAATCACTGGCTTGCAGG 1888
QY 1683 GAAGACGACACTGCTGAGAACGACTACAAAGAACAAAGGTACATGGAATACAGAG 1742
Db 1887 GAAGACGACACTGCTGAGAACGACTACAAAGAACAAAGGTACATGGAATACAGAG 1828
QY 1743 AACTAAGAGGCTTTAGTGAGGACAATTTGGAATTTAGGAATTCGTCCTGACAGAT 1802
Db 1827 AACTAAGAGGCTTTAGTGAGGACAATTTGGAATTTAGGAATTCGTCCTGACAGAT 1768
QY 1803 TCGACTTCTTCCACATCGAATCAACCGGTGGAAGAGGTCTTAACCGTAAACTCTCTCAT 1862
Db 1767 TCGACTTCTTCCACATCGAATCAACCGGTGGAAGAGGTCTTAACCGTAAACTCTCTCAT 1708
QY 1863 CGTCGCGTGAGACTCTTGCCTCTAGTGTAAATTTTGTCTGACCATATAATCTGTTT 1922
Db 1707 CGTCGCGTGAGACTCTTGCCTCTAGTGTAAATTTTGTCTGACCATATAATCTGTTT 1648
QY 1923 TCATGATGACTGTAACGTGTTATGTCTATCTGTTGGGTCTATATAGTTTCGCTCTCGTTT 1982
Db 1647 TCATGATGACTGTAACGTGTTATGTCTATCTGTTGGGTCTATATAGTTTCGCTCTCGTTT 1588
QY 1983 TGCATCTGTGTATATATGCTGAGGTGCTTCAACAAATGTTGTAACAATTTGAACC 2042
Db 1587 TGCATCTGTGTATATATGCTGAGGTGCTTCAACAAATGTTGTAACAATTTGAACC 1528
QY 2043 AATGGTATACAGATTTGTAATATATATTTATGTACATCAACAATAA 2088
Db 1527 AATGGTATACAGATTTGTAATATATATTTATGTACATCAACAATAA 1482

RESULT 9
US-08-989-478-11
; Sequence 11 Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/S-21214/PI/CGC1911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1608 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1608
; OTHER INFORMATION: /product= "Altered form of NIM1"
; OTHER INFORMATION: /note= "C-terminal deletion compared to wild-type NIM1."
US-08-989-478-11

Query Match 76.3%; Score 1605; DB 2; Length 1608;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACTTGTAT 110
Db 1 GATCTCTTTAAATTTGTGAATTTCAATTCATCGGAACCTGTTGATGGACACCACTTGTAT 60
QY 111 GGATTCGCCGATTCCTTATGAAATFACAGCAGCACTAGTTTCGTCGCTACCGATACACCGAC 170
Db 61 GGATTCGCCGATTCCTTATGAAATFACAGCAGCACTAGTTTCGTCGCTACCGATACACCGAC 120
QY 171 TCCTCTATTGTTTATCTGCGCCGCGGAAAGTACTCACCAGGACCTGATGTATCTGCTCTG 230
Db 121 TCCTCTATTGTTTATCTGCGCCGCGGAAAGTACTCACCAGGACCTGATGTATCTGCTCTG 180
QY 231 CAATTCGCTCTCCAAACAGCTTCGAATCCGTTTGTACTCGCCGAGATTTCTACAGCGAC 290
Db 181 CAATTCGCTCTCCAAACAGCTTCGAATCCGTTTGTACTCGCCGAGATTTCTACAGCGAC 240
QY 291 GCTAAGCTGTTCTCTCCGACGCCCGGGAAGTTTCTTTCCACCGGTGCGTTTGTTCAGCG 350
Db 241 GCTAAGCTGTTCTCTCCGACGCCCGGGAAGTTTCTTTCCACCGGTGCGTTTGTTCAGCG 300
QY 351 AGAAGCTCTTTCTTCAAGAGCGCTTTTAGCGCGCTTAAAGAGGAGAAAGACTCCCAACAC 410
Db 301 AGAAGCTCTTTCTTCAAGAGCGCTTTTAGCGCGCTTAAAGAGGAGAAAGACTCCCAACAC 360
QY 411 ACCGCCCGCTGAGCTCGAGCTTAAAGAGATTTGCCAAGATTTACGAAGTTCGGTTTCGAT 470
Db 361 ACCGCCCGCTGAGCTCGAGCTTAAAGAGATTTGCCAAGATTTACGAAGTTCGGTTTCGAT 420
QY 471 TCGGTTGTGACTGTTTTCGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCTAAAGGA 530
Db 421 TCGGTTGTGACTGTTTTCGCTTATGTTTACAGCAGCAGAGTGAGACCGCCGCTAAAGGA 480
QY 531 GTTTCTGAATCGCAGACGAGAAATTTGCTGCACGTGCTTGCCTGCGCGCGGCGGTTCGATTC 590

Db 481 GTTCTGAATGCGCAGACGAGATTGCTGCCACGTTGGCTTGGCGCGCGGTGGATTTC 540
QY 591 ATGTTGGAGGTTCTCTATTGTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTAT 650
Db 541 ATGTTGGAGGTTCTCTATTGTTGGCTTTTCATCTTCAAGATCCCTGAATTAATTACTCTCTAT 600
QY 651 CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACATC 710
Db 601 CAGAGGCACTTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTGGTTATACATC 660
QY 711 AAGCTTGCTAATATATATGTTGTAAGCTTGTATGAAGCTATTTGATAGATGTAAGAGATT 770
Db 661 AAGCTTGCTAATATATGTTGTAAGCTTGTATGAAGCTATTTGATAGATGTAAGAGATT 720
QY 771 ATTGTCAAGTCTAATGTAGATATGTTAGTCTTGAAGGTCATTGCGGGAAGAGCTTGT 830
Db 721 ATTGTCAAGTCTAATGTAGATATGTTAGTCTTGAAGGTCATTGCGGGAAGAGCTTGT 780
QY 831 AAAGAGATAATTGTAGACGCTAAAGAGCTTGGTTGGAGGTACCTAAAGTAAAGAAACAT 890
Db 781 AAAGAGATAATTGTAGACGCTAAAGAGCTTGGTTGGAGGTACCTAAAGTAAAGAAACAT 840
QY 891 GTCCTGAATGTACATAGGCACTTGAAGGCACTTGGCTCGGATGATATTCAGTTAGTCTTTTG 950
Db 841 GTCCTGAATGTACATAGGCACTTGGCTCGGATGATATTCAGTTAGTCTTTTG 900
QY 951 AAAGAGATCACCAATCTAGATGATGCTGTGCTTTCATTTGCTGTTGATATTCG 1010
Db 901 AAAGAGATCACCAATCTAGATGATGCTGTGCTTTCATTTGCTGTTGATATTCG 960
QY 1011 AATGTGAAGACCGACACAGATCTTTTAAACTTGATCTTCCGATGTCACCATAGGAAT 1070
Db 961 AATGTGAAGACCGACACAGATCTTTTAAACTTGATCTTCCGATGTCACCATAGGAAT 1020
QY 1071 CCGAGGGGATATAGGTTGCTTTCATGTTGCTGCGATGCGGAGGACACAAATTTGACTA 1130
Db 1021 CCGAGGGGATATAGGTTGCTTTCATGTTGCTGCGATGCGGAGGACACAAATTTGACTA 1080
QY 1131 TCTCTATTGGAAGGAGTGAAGTGCATCAGAACCACTTTGGAAGGTAGAACCGCACTC 1190
Db 1081 TCTCTATTGGAAGGAGTGAAGTGCATCAGAACCACTTTGGAAGGTAGAACCGCACTC 1140
QY 1191 ATGATCGCAAAACAGGCACTATGCGGTTGAATGTAATATATCCCGGAGCAATGCAAG 1250
Db 1141 ATGATCGCAAAACAGGCACTATGCGGTTGAATGTAATATATCCCGGAGCAATGCAAG 1200
QY 1251 CATCTCTCAAGGCGCACTATGTTAGAAATCTAGAGCAAGAACACAAACGAGAACAA 1310
Db 1201 CATCTCTCAAGGCGCACTATGTTAGAAATCTAGAGCAAGAACACAAACGAGAACAA 1260
QY 1311 ATTCTTAGAGATGTTCTCCCTCTTTTTCAGTGGCGCGGATGAATGAAGATGACGCTG 1370
Db 1261 ATTCTTAGAGATGTTCTCCCTCTTTTTCAGTGGCGCGGATGAATGAAGATGACGCTG 1320
QY 1371 CTCGATCTGAAAATAGAGTTGCACTTGTCTCAAGCTCTTTTTCAGGGAAGCAAGCT 1430
Db 1321 CTCGATCTGAAAATAGAGTTGCACTTGTCTCAAGCTCTTTTTCAGGGAAGCAAGCT 1380
QY 1431 GCAATGGAGATGCGGCAATGAAGGACATGTCAGTTCACTAGTACCTAGCTCGAGCCT 1490
Db 1381 GCAATGGAGATGCGGCAATGAAGGACATGTCAGTTCACTAGTACCTAGCTCGAGCCT 1440
QY 1491 GACCGTCTCACTGTTACGAAGAACATACCGGTTGTAAAGATAGACCTTTTCAAGATC 1550
Db 1441 GACCGTCTCACTGTTACGAAGAACATACCGGTTGTAAAGATAGACCTTTTCAAGATC 1500
QY 1551 CTAGAGACCAATCAAGTAGACTTAAGCGCTTTTCTAAACCGTGAAGTGGGGAACGA 1610
Db 1501 CTAGAGACCAATCAAGTAGACTTAAGCGCTTTTCTAAACCGTGAAGTGGGGAACGA 1560
QY 1611 TTCTTCCCGCGCTGTTCCGCGAGTGTCCGACCAAGATTATGAAGTGT 1655
|||||
Db 1561 TTCTTCCCGCGCTGTTCCGCGAGTGTCCGACCAAGATTATGAAGTGT 1605

RESULT 10
US-08-996-685-11
; Sequence 11, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Ruess, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1608 base pairs
; TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1608
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-996-685-11

```

Query Match		76.3%;	Score 1605;	DB 3;	Length 1608;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1605; Conservative		0;	Mismatches	0;	Indels 0; Gaps
QY	51	GATCTCTTAAATTTGTGAATTTCAATTATCGAAGCCTGTTGATGAGACACCACTATTGAT	110		
DB	1	GATCTCTTAAATTTGTGAATTTCAATTATCGAAGCCTGTTGATGAGACACCACTATTGAT	60		
QY	111	GGATTCCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTTCGTTACGATTAACACCGAC	170		
DB	61	GGATTCCCGATTCTTATGAAATCAGCAGCACTAGTTTCGTTCGTTACGATTAACACCGAC	120		
QY	171	TCCTCTATTGTTTATCTGGCCGCCGAACAGTACTCACCGGACCTGATGATCTGCTCTG	230		
DB	121	TCCTCTATTGTTTATCTGGCCGCCGAACAGTACTCACCGGACCTGATGATCTGCTCTG	180		
QY	231	CAATTGCTCTCCAACAGCTTCGAATCCGCTTTGACTCCGCCGGATGATTCTACAGCGAC	290		
DB	181	CAATTGCTCTCCAACAGCTTCGAATCCGCTTTGACTCCGCCGGATGATTCTACAGCGAC	240		
QY	291	GCTAAGCTTGTCTCTCCGACGCCGGGAAGTTTCTTCCACCGTGCCTTTTGTCAAGCG	350		
DB	241	GCTAAGCTTGTCTCTCCGACGCCGGGAAGTTTCTTCCACCGTGCCTTTTGTCAAGCG	300		
QY	351	AGAAGCTCTTTCCTCAGAGCGCTTTAGCCGCCCTAAGAGAGAGAAAGACTCCCAACAC	410		
DB	301	AGAAGCTCTTTCCTCAGAGCGCTTTAGCCGCCCTAAGAGAGAGAAAGACTCCCAACAC	360		
QY	411	ACCGCCGCCGTGAAGCTCGAGCTTAAGAGATTTGCCAAGGATTACCAAGTTCGGTTTCGAT	470		
DB	361	ACCGCCGCCGTGAAGCTCGAGCTTAAGAGATTTGCCAAGGATTACCAAGTTCGGTTTCGAT	420		
QY	471	TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTAAAGA	530		
DB	421	TCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTAAAGA	480		
QY	531	GTTCCTGAATCGGCAGACGAGAAATGCTGCCAGTGGCTTCCCGCGCGGGTGGATTTC	590		
DB	481	GTTCCTGAATCGGCAGACGAGAAATGCTGCCAGTGGCTTCCCGCGCGGGTGGATTTC	540		
QY	591	ATGTTGGAGGTTCTCTATTTGGCTTTCATCTCAAGATCGCTCAATTAATTACTCTCTAT	650		
DB	541	ATGTTGGAGGTTCTCTATTTGGCTTTCATCTCAAGATCGCTCAATTAATTACTCTCTAT	600		
QY	651	CAGAGGCACCTATTGGAGCTTGTAGACAAAGTTGTTATAGAGACACATTTGGTTATACTC	710		
DB	601	CAGAGGCACCTATTGGAGCTTGTAGACAAAGTTGTTATAGAGACACATTTGGTTATACTC	660		
QY	711	AAGCTTGCTAATAFATATGTGGTAAAGCTTGTATGAAGCTATTGATAGATCTAAAGAGATT	770		
DB	661	AAGCTTGCTAATAFATATGTGGTAAAGCTTGTATGAAGCTATTGATAGATCTAAAGAGATT	720		
QY	771	ATTGTCGAAGCTTAATGTAGATATGTTAGTCTTCAAAAGTCATTGCCGGAAGAGCTTGTT	830		
DB	721	ATTGTCGAAGCTTAATGTAGATATGTTAGTCTTCAAAAGTCATTGCCGGAAGAGCTTGTT	780		
QY	831	AAAGAGATAAATTTGATAGACGTAAGAGAGCTTGTTTGGAGGTACCTAAAGTAAAGAAACAT	890		
DB	781	AAAGAGATAAATTTGATAGACGTAAGAGAGCTTGTTTGGAGGTACCTAAAGTAAAGAAACAT	840		
QY	891	GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG	950		
DB	841	GTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG	900		

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/989, 478
APPLICATION NUMBER: US/08/989, 478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034, 379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034, 382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034, 730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035, 021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035, 022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
OTHER INFORMATION: /product= "Altered form of NIM1"
OTHER INFORMATION: /note= "N-terminal deletion compared to wild-type NIM1"
OTHER INFORMATION: sequence."
US-08-989-478-9

Query Match 75.78; Score 1592.8; DB 2; Length 1597;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	466	TCGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTA	525
Db	2	TGGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCGCTA	61
Qy	526	AAGAGTTTCTGAATGCCAGACAGAGAAATGCTGCCACGTGGCTTGCCGCCGCGCGGTGG	585
Db	62	AAGAGTTTCTGAATGCCAGACAGAGAAATGCTGCCACGTGGCTTGCCGCCGCGCGGTGG	121
Qy	586	ATTTTCATGTTGGAGTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGGAATTAATTA	645
Db	122	ATTTTCATGTTGGAGTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGGAATTAATTA	181
Qy	646	TCTATCAGAGGCACCTTATGGACCTTGTAGACAAAGTTGTTATAGAGGCACACATTTGGTTA	705
Db	182	TCTATCAGAGGCACCTTATGGACCTTGTAGACAAAGTTGTTATAGAGGCACACATTTGGTTA	241
Qy	706	TACTCAAGCTTGCATATATATGTTGTTAAAGCTTGTATGAAGCTATTTGGATAGATGTAAG	765
Db	242	TACTCAAGCTTGCATATATATGTTGTTAAAGCTTGTATGAAGCTATTTGGATAGATGTAAG	301
Qy	766	AGATTATGCAAGCTCAATGTAGATATGGTTAGTCTTTGAAAAGTCAATGCCGGAAGAGC	825
Db	302	AGATTATGCAAGCTCAATGTAGATATGGTTAGTCTTTGAAAAGTCAATGCCGGAAGAGC	961

Qy	826	TTGTTAAAGAGATAATTGATAGACGTAAGAGAGCTTGCTTTGGAGGTACCTAAAGTAAAGA	885
Db	362	TTGTTAAAGAGATAATTGATAGACGTAAGAGAGCTTGCTTTGGAGGTACCTAAAGTAAAGA	421
Qy	886	AACATGCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTCG	945
Db	422	AACATGCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTCG	481
Qy	946	TTTGAAGAGGATCACACCAATCTAGATGATGCGGTGCTCTTTCATTTTCGCTGTTGCAT	1005
Db	482	TTTGAAGAGGATCACACCAATCTAGATGATGCGGTGCTCTTTCATTTTCGCTGTTGCAT	541
Qy	1006	ATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTTGGCGATGTCAACCAT	1065
Db	542	ATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTGATCTTGGCGATGTCAACCAT	601
Qy	1066	GGATCCGAGGGGATATACGGTGTCTCATGTTGCTCGATGCGAAGAGGACCAATTTGA	1125
Db	602	GGATCCGAGGGGATATACGGTGTCTCATGTTGCTCGATGCGAAGAGGACCAATTTGA	561
Qy	1126	TACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAACAACTTTGGAAGGTAGAAGCG	1185
Db	662	TACTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAACAACTTTGGAAGGTAGAAGCG	721
Qy	1186	CACATCATGATCGAAACAAAGCCACTATGCGGTGGAATGTAATATATCCCGAGCAAT	1245
Db	722	CACATCATGATCGAAACAAAGCCACTATGCGGTGGAATGTAATATATCCCGAGCAAT	781
Qy	1246	GCAAGCATTTCTCTCAAAGCCGACTATGTGTAGAAATCTAGAGCAAGAACCAACGAG	1305
Db	782	GCAAGCATTTCTCTCAAAGCCGACTATGTGTAGAAATCTAGAGCAAGAACCAACGAG	841
Qy	1306	AACAAATTCCTAGAGATGTTCTCCCTCTTTTGGAGTGGCGGCGGATGAATTTGAAGATGA	1365
Db	842	AACAAATTCCTAGAGATGTTCTCCCTCTTTTGGAGTGGCGGCGGATGAATTTGAAGATGA	901
Qy	1366	CGCTGCTCGATCTTGAAATAGAGTTGCACCTTGCTCAAGCTCTTTTCCAAAGGAGCAC	1425
Db	902	CGCTGCTCGATCTTGAAATAGAGTTGCACCTTGCTCAAGCTCTTTTCCAAAGGAGCAC	961
Qy	1426	AAGCTCAATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCG	1485
Db	962	AAGCTCAATGGAGATCGCGGAAATGAAGGGAACATGTGAGTTTCATAGTACTAGCCTCG	1021
Qy	1486	AGCTGACCGCTCTCACTGCTACAGAGAACATCAACCGGTTGTAAGATAGCACCTTTCA	1545
Db	1022	AGCTGACCGCTCTCACTGCTACAGAGAACATCAACCGGTTGTAAGATAGCACCTTTCA	1081
Qy	1546	GAATCTCTAGAAGAGCATCAAGTATGAAAGCGCTTTCTAAACCGTGGAACTCGGA	1605
Db	1082	GAATCTCTAGAAGAGCATCAAGTATGAAAGCGCTTTCTAAACCGTGGAACTCGGA	1141
Qy	1606	AAGGATTTCTTCCCGCGCTGTTTCGGCAGTCTCGACAGATTATGAACCTGTGAGGACTTGA	1665
Db	1142	AAGGATTTCTTCCCGCGCTGTTTCGGCAGTCTCGACAGATTATGAACCTGTGAGGACTTGA	1201
Qy	1666	CTCAACTGCGTTCGCGAAGAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGT	1725
Db	1202	CTCAACTGCGTTCGCGAAGAGACGACACTGCTGAGAAACGACTACAAAAGAGCAAGGT	1261
Qy	1726	ACATGGAATACAAAGAGACACTAAAGAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAA	1785
Db	1262	ACATGGAATACAAAGAGACACTAAAGAGCGCTTTAGTGAGGACAAATTTGGAATTAGGAA	1321
Qy	1786	ATTGCTCCCTGACAGATTTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGTCTTA	1845
Db	1322	ATTGCTCCCTGACAGATTTCGACTTCTTCCACATCGAAATCAACCGGTGGAAAGAGTCTTA	1381
Qy	1846	ACGTTAAACTCTCTCATCGTTCGCGTGAGACTCTTTGCGCTCTTAGTGTAAATTTTTCGT	1905
Db	1382	ACGTTAAACTCTCTCATCGTTCGCGTGAGACTCTTTGCGCTCTTAGTGTAAATTTTTCGT	1441
Qy	1906	ACCATATAATTCTGTTTTCATGATGACTTAATCTTTTATGTTATGTTGCGTTCATAT	1965

|||||
Db 1442 ACCATAATCTGTTTTCATGATGACTGAACGTGTTATGTTATGCTATCGTTGGCGTCATAT 1501
QY 1966 AGTTTCGCTCTTGGTTTTCATGCTGTGATATTGCTGTCAGGTGCTGTTCAAAACAATG 2025
Db 1502 AGTTTCGCTCTTGGTTTTCATGCTGTGATATTGCTGTCAGGTGCTGTTCAAAACAATG 1561
QY 2026 TTGTAAACAATTTGAACCAATGGTATACAGATTGTA 2061
Db 1562 TTGTAAACAATTTGAACCAATGGTATACAGATTGTA 1597

RESULT 12

US-08-996-685-9
Sequence 9, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Russ, Wilhelm
APPLICANT: Knauf-Beiter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6031153th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,378
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy

REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
OTHER INFORMATION: /product= "Altered form of NIMI"
OTHER INFORMATION: /note= "N-terminal deletion compared to wild-type NIMI"
US-08-996-685-9
Query Match 75.7%; Score 1592.8; DB 3; Length 1597;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 466 TCGATTTCGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGGCTA 525
Db 2 TGGATTCGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGGCTA 61
QY 526 RAGGAGTTTCTGAATGCGCAGCAGAGAAATGCTGCCAGTGGCTTGGCGCGCGGCTGG 585
Db 62 RAGGAGTTTCTGAATGCGCAGCAGAGAAATGCTGCCAGTGGCTTGGCGCGCGGCTGG 121
QY 586 ATTTTCATGTTGGAGGTTCTCTATTGTTGGCTTTCATCTTCAAGATCCCTGAATTAATCTC 645
Db 122 ATTTTCATGTTGGAGGTTCTCTATTGTTGGCTTTCATCTTCAAGATCCCTGAATTAATCTC 181
QY 646 TCTATCAGAGGCACATTATGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTTGTTA 705
Db 182 TCTATCAGAGGCACATTATGGACGTTGTAGACAAAGTTGTTATAGAGGACACATTTGTTA 241
QY 706 TACTCAAGCTTGCATAATATATGTTGTTAAAGCTTGATGAAGCTTATGATAGATGTTAAAG 765
Db 242 TACTCAAGCTTGCATAATATATGTTGTTAAAGCTTGATGAAGCTTATGATAGATGTTAAAG 301
QY 766 AGATTATTGTCAAGTCTAATGTAGATATGTTAGTCTTTGAAAAGTCATTGCCGGAAGAGC 825
Db 302 AGATTATTGTCAAGTCTAATGTAGATATGTTAGTCTTTGAAAAGTCATTGCCGGAAGAGC 361
QY 826 TTGTTAAAGAGATAATTTGATAGACGTTAAAGAGCTTGGTTGGAGGTACCTTAAAGTAAAGA 885
Db 362 TTGTTAAAGAGATAATTTGATAGACGTTAAAGAGCTTGGTTGGAGGTACCTTAAAGTAAAGA 421
QY 886 AACATGCTCTGAATGTACATGAAGCAGCTTGACTCGGATGATATTGAGTTAGTCAAGTTGC 945
Db 422 AACATGCTCTGAATGTACATGAAGCAGCTTGACTCGGATGATATTGAGTTAGTCAAGTTGC 481
QY 946 TTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTCTCTTCATTTTCGCTGTTCAT 1005
Db 482 TTTTGAAGAGGATCACACCAATCTAGATGATGCGTGTCTCTTCATTTTCGCTGTTCAT 541
QY 1006 ATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTTGATCTTCCGATGTCACACCTA 1065
Db 542 ATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTTGATCTTCCGATGTCACACCTA 601
QY 1066 GGAATCCGAGGGGATATACGGTGTCTTCATGTTGTCGATCGGAAGGAGGACCAATTTGA 1125
Db 602 GGAATCCGAGGGGATATACGGTGTCTTCATGTTGTCGATCGGAAGGAGGACCAATTTGA 661
QY 1126 TACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAGCAACTTTTGGAAAGGTAGACCG 1185
Db 662 TACTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAGCAACTTTTGGAAAGGTAGACCG 721
QY 1186 CACTCATGNTCCAAACAACAGCCACTATGGCGGTTGAATTAATAATATCCCGAGGCAAT 1245

RESULT 13

```

US-08-989-478-13
; Sequence 13, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS
; TITLE OF INVENTION: DISEASE RESISTANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

```

Query Match	56.5%;	Score 1188.4;	DB 2;	Length 1194;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1189; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	466	TCGATT	CGGTGTTGAC	TGTTTTGGCCTAT	GTGTACACGACGAGT	GAGACCGCGCCTA	5255
Db	2	TGGATT	CGGTGTTGAC	TGTTTTGGCCTAT	GTGTACACGACGAGT	GAGACCGCGCCTA	61
Qy	526	AAGGAGT	TTCTGAATCGCAGACAGAGAA	TTCCTGCCACGTGGCTT	GCCGGCGCGGTGG		5855
Db	62	AAGGAGT	TTCTGAATCGCAGACAGAGAA	TTCCTGCCACGTGGCTT	GCCGGCGCGGTGG		1215
Qy	586	ATTTCATGTTGGAGGT	TCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAAT	TACTC			6455
Db	122	ATTTCATGTTGGAGGT	TCTCTATTGGCTTTCATCTTCAAGATCCCTGAATTAAT	TACTC			1815
Qy	646	TCTATCAGAGC	ACTTATTTGGACGTTGTAGACAAAGTTGTTATAGAGGACACAT	TGGTTA			7055
Db	182	TCTATCAGAGC	ACTTATTTGGACGTTGTAGACAAAGTTGTTATAGAGGACACAT	TGGTTA			2415


```

1022 AGCCTGACCGTCTCACTGGTACGAAGAACAATCACCGGGTGTAAAAGATAGCACCTTTCA 1081
1546 GAATCCTAGAGAGCATCAAGTAGACTAAAAACGGCTTCTTAAACCGTGGAACTCGGGA 1605
1082 GAATCCTAGAGAGCATCAAGTAGACTAAAAACGGCTTCTTAAACCGTGGAACTCGGGA 1141
1606 AACGATTCTCCCGCGCTGTTCGGCAGTGTCTGACACAGATTATGAACCTGT 1655
1142 AACGATTCTCCCGCGCTGTTCGGCAGTGTCTGACACAGATTATGAACCTGT 1191

RESULT 15
US-08-989-478-15
: Sequence 15, Application US/08989478
: Patent No. 5986082
: GENERAL INFORMATION:
: APPLICANT: Uknes, Scott
: APPLICANT: Hunt, Michelle
: APPLICANT: Steiner, Henry-York
: APPLICANT: Ryals, John
: TITLE OF INVENTION: ALTERED FORMS OF THE NM1 GENE CONFERRING
: TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: NO. 5986082artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NO. 5986082th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/989,478
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/033,177
: FILING DATE: 13-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,379
: FILING DATE: 27-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,382
: FILING DATE: 27-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/034,730
: FILING DATE: 10-JAN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/035,021
: FILING DATE: 10-JAN-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/035,022
: FILING DATE: 10-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 541-8587
: TELEFAX: (919) 541-8689
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 786 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:

```



```
; NAME/KEY: CDS
; LOCATION: 1..786
; OTHER INFORMATION: /product= "Altered form of NIM1"
; OTHER INFORMATION: /note= "Ankyrin domains of NIM1."
US-08-989-478-15

Query Match      37.1%; Score 781.4; DB 2; Length 786;
Best Local Similarity 99.9%; Pred. No. 3.3e-213;
Matches 782; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 399 GACTCCAACAACACCAGCGCGGCGGAGCTCGAGCTTAAGAGATTGCCAAGGATTACGAA 458
Db      |||||||
Qy 459 GTCGGTTTCGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCG 518
Db      |||||||
Qy 64 GTCGGTTTCGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCG 123
Db      |||||||
Qy 519 CCGCCTAAAGGAGTTTCTGAATGCGCAGACGAGAAATGCTGCCACGTGGCTTGC CGCGCG 578
Db      |||||||
Qy 124 CCGCCTAAAGGAGTTTCTGAATGCGCAGACGAGAAATGCTGCCACGTGGCTTGC CGCGCG 183
Db      |||||||
Qy 579 GCGGTGATTTCAATGTTGGAGTTCTCTATTTGGCTTTCATCTCAAGATCCCTGAATTA 638
Db      |||||||
Qy 184 GCGGTGATTTCAATGTTGGAGTTCTCTATTTGGCTTTCATCTCAAGATCCCTGAATTA 243
Db      |||||||
Qy 639 ATTACTCTCTATCAGAGGCACCTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACA 698
Db      |||||||
Qy 244 ATTACTCTCTATCAGAGGCACCTATTGGACGTTGTAGACAAAGTTGTTATAGAGGACACA 303
Db      |||||||
Qy 699 TTGGTTTACTCAAGCTTGCTTAATATATGTGTTAAAGCTTGTATGAAGCTATTGGATAGA 758
Db      |||||||
Qy 304 TTGGTTTACTCAAGCTTGCTTAATATATGTGTTAAAGCTTGTATGAAGCTATTGGATAGA 363
Db      |||||||
Qy 759 TGTAAGAGATTATTGTCAAGTCTAATGTAGATATAGTGTAGTCTTGAAAAGTCATTGCCG 818
Db      |||||||
Qy 364 TGTAAAGAGATTATTGTCAAGTCTAATGTAGATATAGTGTAGTCTTGAAAAGTCATTGCCG 423
Db      |||||||
Qy 819 GAAGAGCTTCTTAAAGAGATAATTGTATAGACGTAAGAGCTTGGTTTGGAGGTACCTAAA 878
Db      |||||||
Qy 424 GAAGAGCTTCTTAAAGAGATAATTGTATAGACGTAAGAGCTTGGTTTGGAGGTACCTAAA 483
Db      |||||||
Qy 879 GTAAAGAAACATCTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTC 938
Db      |||||||
Qy 484 GTAAAGAAACATCTCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTC 543
Db      |||||||
Qy 939 AGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGGTGCTCTTTCATTTCCGT 998
Db      |||||||
Qy 544 AGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATCGGTGCTCTTTCATTTCCGT 603
Db      |||||||
Qy 999 GTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTCATCTTGCCGATGTC 1058
Db      |||||||
Qy 604 GTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACTTCATCTTGCCGATGTC 563
Db      |||||||
Qy 1059 AACCATAGGAATCCGAGGGGATATACGGTCTTCATGTTGCTGCGATCGGAAGAGGCCA 1118
Db      |||||||
Qy 664 AACCATAGGAATCCGAGGGGATATACGGTCTTCATGTTGCTGCGATCGGAAGAGGCCA 723
Db      |||||||
Qy 1119 CAATTGATCTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAACCACTTTGGAAAGT 1178
Db      |||||||
Qy 724 CAATTGATCTATCTCTATTGGAAAAAGGTGCAAGTGCATCAGAACCACTTTGGAAAGT 783
Db      |||||||
Qy 1179 AGA 1181
Db      ||
Qy 784 TGA 786
```

Search completed: October 8, 2002, 01:23:14
Job time : 117.761 secs

GenCore version 5.1.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 21:32:09 ; Search time 1642.95 Seconds
(without alignments)
17284.510 Million cell updates/sec

Title: US-08-908-884-2
Perfect score: 2104
Sequence: 1 TCGATCTTTAACCAATCA.....ATAAAAAAAAAAAAAAAAA 2104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpi:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_gss:*
13:	em_gss_inv:*
14:	em_gss_inv:*
15:	em_gss_pln:*
16:	em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	573	27.2	573	9 AV551266	AV551266 AV551266
2	493	23.4	495	9 A1997958	A1997958 701671677
3	378.6	18.0	470	9 AA395706	AA395706 28108 Lam
4	307.8	14.6	338	9 AV557971	AV557971 AV557971
5	305.2	14.5	772	12 BH525927	BH525927 B0GT004TF
6	236	11.2	799	12 BH602085	BH602085 B0HK84TF
7	231.2	11.0	258	10 T22612	T22612 4620 Lambda
8	228.8	10.9	463	12 BH211724	BH211724 SALK_0065
9	212.8	10.1	613	9 AW160235	AW160235 EST290093
10	211.4	10.0	614	10 BG464249	BG464249 EMI_71.D1
11	187.8	8.9	700	10 BM111027	BM111027 EST558563
12	186.8	8.9	654	10 BG124935	BG124935 EST470581
13	172.2	8.2	785	12 BH602094	BH602094 B0HK84TR
14	163.2	7.8	667	10 BG598808	BG598808 EST503708
15	160.6	7.6	455	10 BE493178	BE493178 WHE0570_C
16	154.2	7.3	450	9 AK399343	AK399343 EST309843
17	152.8	7.3	744	10 BG526766	BG526766 63-52 Ste

c	18	145	6.9	629	12	B26306	B26306 F18D8TF IGF
	19	144	6.8	569	9	AW745943	AW745943 WS1_38.H0
	20	140.6	6.7	458	9	BE023215	BE023215 sm70a04.Y
	21	138.2	6.6	736	10	BE435499	BE435499 EST406577
	22	136.8	6.5	547	10	BE918569	BE918569 OVL_8.E08
	23	135.2	6.4	637	10	BG521476	BG521476 10-59 Ste
	24	133	6.3	491	10	BF657743	BF657743 OV2_17_E0
c	25	131.6	6.3	516	9	AW622846	AW622846 EST306916
	26	131	6.2	462	9	AL372473	AL372473 MTBA51C01
	27	128.6	6.1	835	12	BH594302	BH594302 BOHOK24TR
	28	128.2	6.1	588	10	BM307942	BM307942 sak39h08.
	29	124.2	5.9	503	10	BE432768	BE432768 EST399297
	30	115.6	5.5	430	9	AL442277	AL442277 sa66a04.Y
	31	114	5.4	535	9	AW687759	AW687759 NF013805R
c	32	112.6	5.4	781	12	BH483537	BH483537 B0GXP26TF
	33	111.4	5.3	577	10	BM324012	BM324012 P1C1_30.C
c	34	111	5.3	730	10	BI968818	BI968818 GM830005B
	35	108.8	5.2	569	10	BE366197	BE366197 P1L_31.F0
	36	107.6	5.1	595	10	BE801977	BE801977 sr23d08.Y
	37	105.6	5.0	562	10	BE366196	BE366196 P1L_31.F0
	38	105.4	5.0	805	10	BG414779	BG414779 HVSMEK000
	39	104.4	5.0	765	10	BG526883	BG526883 40-96 Ste
	40	103	4.9	539	10	BI210424	BI210424 EST528464
c	41	102.6	4.9	645	9	AW310982	AW310982 sg31b02.x
	42	101.8	4.8	612	9	AI054662	AI054662 coau0001K
	43	96.4	4.6	430	10	BI071038	BI071038 CO51P30U
	44	95.8	4.6	419	10	BI070963	BI070963 CO50P20U
c	45	89.4	4.2	680	9	AW309867	AW309867 sf25g10.x

ALIGNMENTS

RESULT 1
AV551266
LOCUS AV551266 573 bp mRNA linear EST 06-SEP-2000
DEFINITION AV551266 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
CDNA clone RZ123e05R 5', mRNA sequence.
AV551266
ACCESSION AV551266
VERSION AV551266.1 GI:8722679
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 573)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizukazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES
source
1. .573
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="RZ123e05R"
/clone_lib="Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 181 a 104 c 137 g 151 t
ORIGIN
Query Match 27.2%; Score 573; DB 9; Length 573;
Best Local Similarity 100.0%; Pred. No. 9.5e-99;

Matches 573; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 775	TCAAAGTCTAATCTAGATATGGTTAGCTTGAAGAGCTATTCGCGAAGAGCTTGTAAAG	834	
Db 1	TCAAAGTCTAATCTAGATATGGTTAGCTTGAAGAGCTATTCGCGAAGAGCTTGTAAAG	60	
Qy 835	AGATAATTGATAGAGCTAAAGAGCTTGGTTGGAGGTACCTAAAGTAAAGAAACATGTCT	894	
Db 61	AGATAATTGATAGAGCTAAAGAGCTTGGTTGGAGGTACCTAAAGTAAAGAAACATGTCT	120	
Qy 895	CGAATGTACATAGGCACTTGACTCGGATGATATTAGTTAGTCAAGTTGCTTTTGAAG	954	
Db 121	CGAATGTACATAGGCACTTGACTCGGATGATATTAGTTAGTCAAGTTGCTTTTGAAG	180	
Qy 955	AGGATCACACCAATCTAGATGATGGTGTGCTTCATTTGCTCTGTTGCATATTGCAATG	1014	
Db 181	AGGATCACACCAATCTAGATGATGGTGTGCTTCATTTGCTCTGTTGCATATTGCAATG	240	
Qy 1015	TGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGATGTCAACCATAGGAATCCGA	1074	
Db 241	TGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGATGTCAACCATAGGAATCCGA	300	
Qy 1075	GGGATATACGTTGCTTCATGTTGCTGGATCGGAAGAGCCACAATTGATATCTC	1134	
Db 301	GGGATATACGTTGCTTCATGTTGCTGGATCGGAAGAGCCACAATTGATATCTC	360	
Qy 1135	TATTGAAAAAGGTGCAAGTGCATCAGAAAGCACTTTGGAAGGTAGAACCAGCACTCATGA	1194	
Db 361	TATTGAAAAAGGTGCAAGTGCATCAGAAAGCACTTTGGAAGGTAGAACCAGCACTCATGA	420	
Qy 1195	TCGCAAAACCAAGCCACTATGGCGGTTGAATGTAATAATATCCCGAGCAATGCAAGCAATT	1254	
Db 421	TCGCAAAACCAAGCCACTATGGCGGTTGAATGTAATAATATCCCGAGCAATGCAAGCAATT	480	
Qy 1255	CTCTCAAGCCGCACTATGTAGAAATCTAGACGAGCAAGACAAACGAGACAAATTC	1314	
Db 481	CTCTCAAGCCGCACTATGTAGAAATCTAGACGAGCAAGACAAACGAGACAAATTC	540	
Qy 1315	CTAGAGATGTTCTCCCTCTTTTGCAGTGGCGG	1347	
Db 541	CTAGAGATGTTCTCCCTCTTTGCAAGTGGCGG	573	

RESULT 2
AI997958/c 495 bp mRNA linear EST 08-SEP-1999
LOCUS 701671677 A. thaliana, Columbia Col-0, rosette-1 Arabidopsis
DEFINITION thaliana cDNA clone 701671677, mRNA sequence.

ACCESSION AI997958.1 GI:5844863
VERSION AI997958
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 495)
AUTHORS Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobrigha, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
TITLE Arabidopsis thaliana Gene Expression MicroArray
JOURNAL Unpublished (1999)
COMMENT Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers

FEATURES
ORIGIN Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
LOCUS AA395706
DEFINITION 28108 Lambda-PRL2 Arabidopsis thaliana cDNA clone 9905XP 3', mRNA
ACCESSION AA395706
VERSION AA395706.1 GI:2048931
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

source 1..495
/organism="Arabidopsis thaliana"
/cultivar="Columbia Col-0"
/db_xref="taxon:3702"
/clone="701671677"
/clone_lib="A. thaliana, Columbia Col-0, rosette-1"
/tissue_type="rosette"
/dev_stage="4 - 7 weeks"
/note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA library was derived from untreated rosette tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."
BASE COUNT 142 a 109 c 141 t 2 others
ORIGIN

Query Match 23.4%; Score 493; DB 9; Length 495;			
Best Local Similarity 99.6%; Pred. No. 1.4e-83;			
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy 1543	TCAGAATCCTAGAAGAGCATCAAAGTAGACTAAAGCGCTTTCTAAACCGTGGAACTCG	1602	
Db 495	TCAGAATCCTAGAAGAGCATCAAAGTAGACTAAAGCGCTTTCTAAACCGTGGAACTCG	436	
Qy 1603	GGAACCAATTCCTCCCGCGCTGTCGCGAGTGTCCGACAGATTATGAACCTGCGAGCT	1662	
Db 435	GGAACCAATTCCTCCCGCGCTGTCGCGAGTGTCCGACAGATTATGAACCTGCGAGCT	376	
Qy 1663	TGACTCAACTGGCTTCGGGAGAGCAGACACTGCTGAGAACGACTACAAAAGAACGAAA	1722	
Db 375	TGACTCAACTGGCTTCGGGAGAGCAGACACTGCTGAGAACGACTACAAAAGAACGAAA	316	
Qy 1723	GGTACATGGAATACAAAGAGACACTAAAGAGGCGCTTTAGTGAGGACAATTTGGAATTAG	1782	
Db 315	GGTACATGGAATACAAAGAGACACTAAAGAGGCGCTTTAGTGAGGACAATTTGGAATTAG	256	
Qy 1783	GAAATTCGTCCTGACAGATTCGACTTCTCCACATCGAATCAACCGGTGGAAGAGGT	1842	
Db 255	GAAATTCGTCCTGACAGATTCGACTTCTCCACATCGAATCAACCGGTGGAAGAGGT	196	
Qy 1843	CTAACCGTAAACTCTCATCGTCGTCGAGACTCTTGCTCTTATGCTAAATTTTTC	1902	
Db 195	CTAACCGTAAACTCTCATCGTCGTCGAGANTCTTGCCCTCTTATGCTAAATTTTTC	136	
Qy 1903	TGTACCATATAAATTTCTGTTTTCATGATGACTGTAACCTGTTATGCTATCGTGGCGTCA	1962	
Db 135	TGTACCATATAAATTTCTGTTTTCATGATGACTGTAACCTGTTATGCTATCGTGGCGTCA	76	
Qy 1963	TATAGTTTCGCTCTCGTTTTCGATCCTGCTATTATTCGTCAGGTCGCTTCAACAA	2022	
Db 75	TATAGTTTCGCTCTCGTTTTCGATCCTGCTATTATTCGTCAGGTCGCTTCAACAA	16	
Qy 2023	ATGTTGTAACAATTT 2037		
Db 15	ATGTTGTAACAATTT 1		

RESULT 3
AA395706
LOCUS AA395706
DEFINITION 28108 Lambda-PRL2 Arabidopsis thaliana cDNA clone 9905XP 3', mRNA
ACCESSION AA395706
VERSION AA395706.1 GI:2048931
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

DEFINITION BOGT004TF BOGT Brassica oleracea genomic clone BOGT004, DNA sequence.
ACCESSION BH525927
VERSION BH525927.1 GI:17734012
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
REFERENCE
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOGT004TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: Sheared ends.
Location/Qualifiers
source
1..772
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BOGT004"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 199 a 187 c 176 g 210 t
ORIGIN
Query Match 14.5%; Score 305.2; DB 12; Length 772;
Best Local Similarity 69.8%; Pred. No. 5e-48;
Matches 412; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
QY 802 TTGAAAAGTCATTCGCGAAGAGCTGTGTTAAAGAGATAATTGATAGACGTAAGAGCTTG 861
DB 772 TCGACAAGTCTTTACCCCAAGACATGCTCAACAGAGTCCCGACATCCGCAAGAGCTCG 713
QY 862 GTTTGGAGGTCAATAAAGTAAAGAACATGCTCGAATGTACATAAGGCACCTTGACTCGG 921
DB 712 GTCTCGAGCCGCGGACCGGATAAACATGCTCATGAACATATACAAGGCCCTTGACTCCG 653
QY 922 ATGATATTGAGTGTAGTCAAGTTGCTTTTGAAGAGGATCACCAATCTAGATGCGGT 981
DB 652 ACGATGTTGAGCTGTGCAAGTCTTTTGACAGAGGACACACGAGTCTAGACGCGCT 593
QY 982 GTGCTCTTCATTTTCGCTGTGTCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAC 1041
DB 592 ACGTCTTCACTACGCTGTGTCATCTCGATGTGAGAGCGGCTCTGATCTCATTTGACA 533
QY 1042 TTGATCTTGGCGATGTCAACATAGGAATCCGAGGGGATATACGGTCTTCATGTTGCTG 1101
DB 532 TCGAGCTCGCTGACGTGGACCATAGAAACCCGAGGGGATACACGGCGCTTCACGTTGCTG 473
QY 1102 CGATCGGAAGGAGCCACATTTGATCTATCTATTGGAAGAGGTGCAAGTGCATCAG 1161
DB 472 CGATGCGCAACGAGCGAAGCTATGTTTATTTATTTGACTAAGAGTGGGAATTCGCTCGG 413
QY 1162 AAGCAACTTTTGAAGGTAGAACCGCACTCATGATCGCAAAACAGGCACATATGGCGGTTG 1221
DB 412 AGACGAGCTTTGAGGTTAGAACCGCTCTGTTGATTCGGAAGAGGCTCACTAAGAGCTTCGG 353
QY 1222 AATGTAATAATATCCCGAGCAATGCAAGCATTTCTTCAAAAGCCGACATGTGTAGAAA 1281
DB 352 AGTAAATGCTAGTACGAGCAAGGAGGAGCTTCTCTGTAAGAGGAGGCTATGATAGAGG 293
QY 1282 TACTAGACGAAGAGCAACAGAGCAAAATTCCTAGAGATGTTCTCCCTCTTTTGCAG 1341

DB 292 TACTAGACATCGGTGTAACCTAGGTAGCTTGCCTAGAGATGAGTTACTTCTTTCAG 233
QY 1342 TGGCGCGCATGAATTGAAGATGACGCTGCTCGATCTTTGAAAAATAGAGTT 1391
DB 232 CTACTCCTGATGAATTGAGATGAGGCTGCTCTATCTTTGAAAACAGAGGT 183
RESULT 6
LOCUS BH602085/c
DEFINITION BOHKB84TF BOHK Brassica oleracea genomic clone BOHKB84, DNA sequence.
ACCESSION BH602085
VERSION BH602085.1 GI:17854531
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
REFERENCE
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOHKB84TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: Sheared ends.
Location/Qualifiers
source
1..799
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BOHKB84"
/clone_lib="BOHK"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 251 a 164 c 165 g 219 t
ORIGIN
Query Match 11.2%; Score 236; DB 12; Length 799;
Best Local Similarity 75.6%; Pred. No. 6.4e-35;
Matches 360; Conservative 0; Mismatches 105; Indels 11; Gaps 5;
QY 1591 CGCTGGAACTCGGAAAGGATTTCTT-CCCGGCGCTGTTCCGGAGTCTCGACAGATTATG 1649
DB 761 CAGTGAATTCCGGAACGCTTCTTCCCACGCTGTTCCGAAGTCTCGATGATATTGTG 702
QY 1650 AACTGTGAGGACTTGACTCAACTGCTTCCGGAGAGACACACTGCTGAGAAACGACTA 1709
DB 701 GACTGTGAGGACTTGACTATACTGCTCTCTGTAAGAAGACACTCTCTGAGCAACGACAA 642
QY 1710 CAAAAGAGCAAGGTACATGGAATACAAGACACATAAAGAGGCGCTTTAGTGAGGAC 1769
DB 641 CAAAAGAGCAGAGGTTTATGGAATATACAGAGATTGTTCAATGGCGTTTGTAAAGAC 582
QY 1770 AATTTTGGAAATTAGGAATTCGTCCTCGACAGATTTCGACTTCTTCCACATCGAAATCAAC 1829
DB 581 AAGGAGGATCTTGGAAAGTCGTCCTCTCAGCTTCTCTTCTTCCACATCCAAATTAAC 522
QY 1830 GGTGGAAGAGGCTTAACCGTAAACTCTCTCATCTGCTCGTGAGACTCTTGCCCTCTTA 1889
DB 521 GGTAAAGAGGCTTATTGCTAAACCCCTCTACCGGCGCTCGGTGACATATTGTTTC--G 464
QY 1890 GTGTAATTTTCTGCTGACCATAATAATTTCTGTTT---TCATGATGACTGTAATGTTTATG 1946

QY 1092 CATGTTGCTGGATCGGAAGAGCCACAATTGATACCTATCTATTGGAAAAAGGTGCA 1151
Db 343 CATGTTGCTGGATCGGAAGAGCCGAAGTTGATAATATCTTTGTAATGAAGGGCA 284
QY 1152 AGTCATCAGAAAGCAACTTTTGAAGGTAGAACCGCACTCATGATCGCAAAACAAGCCACT 1211
Db 283 AATATTTTAGACACAACTATGGATGGTAGAACCGCTTTAGTGTATGTAACAGCACTCACT 224
QY 1212 ATGGCGGTTGAATGTAATAATATCCGAGCAANTGCRAGCATCTCTCAAGGCCGACTA 1271
Db 223 AAGCGGATGACTACAAACCTAGTAGCGGAGCGGTAGCGCTTCTCGAAAGCGGATTA 164
QY 1272 TGTGTAGAAATAGTAGACAAGACAAACGAGAACAAAT---TCCTAGAGATGTTTCT 1328
Db 163 TGCATAGAGGTACTTGACATGAACAAACTAGATATTTGTCGCCTATAGAGGCTTCA 104
QY 1329 CCCTCTTTGAGTGGCGGCGCATGAATTGAAGATGAGCGTCTCGATCTTGAATAAGA 1388
Db 103 CTTTCTCTTCAGTAACCTCCAGAGAGTTGAGGATGAGGTTGCTCTATTATGAAAAACCGA 44
QY 1389 GTTGCACTTGT 1400
Db 43 GGTATGCTTTCT 32

RESULT 9
LOCUS AW160235 613 bp mRNA linear EST 18-MAY-2001
DEFINITION EST290093 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT119 similar to A. thaliana transcription factor inhibitor I kappa B homolog, mRNA sequence.
ACCESSION AW160235
VERSION AW160235.1 GI:6279769
KEYWORDS EST.
SOURCE Lycopersicon pennellii.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 613)
AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A. L., Lakey, J., Holt, J. E., Liang, F., Hansen, T. S., Updon, J., Ronning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nierman, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
TITLE Generation of ESTs from wild tomato (Lycopersicon pennellii) trichomes
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
3 prime sequence.

FEATURES
source
1..613
/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT119"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
BASE COUNT 159 a 148 c 107 g 199 t
ORIGIN

Query Match 10.18; Score 212.8; DB 9; Length 613;
Best Local Similarity 63.6%; Pred. No. 1.7e-30;

Matches 341; Conservative 0; Mismatches 192; Indels 3; Gaps 1;
QY 1287 GACCAAGACACAAACGAGACAAATTCCTAGAGATGTTCCCTCCCTCTTTTCAGGTGGCG 1346
Db 612 GAGCAAGCAGAAAGAGAGATCCACTACTAGGAGAAGCTTCATTATCTCTTCTATGGCA 553
QY 1347 GCCGATGAATTAAGATGACGCTGCTCGATCTTTGAAATAGAGTTGCATCTGCTCAACCT 1406
Db 552 GCGATGATTTGGTATGAAGCTGTTATACCTTGAAATAGAGTTGGTCTGGCTAACTC 493
QY 1407 CTTTTTCCAAAGGACACAAAGCTGCAATGGAGATCCGCGAAATGAAGGACACATGTGAG 1466
Db 492 CTTTTTCCCATGGAAGCAAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACGCTCGAA 433
QY 1467 TCCATAGTACTAGCTCGAGCCTGACCGCTCTCACCTGTCAGGAGAGACATCACCGGCT 1526
Db 432 TTACCCCTGGCTAGCAT---GAGGAAGAAGATAGCTGATGCACAGAGGACACACAGTGGAT 376
QY 1527 GTAAGATAGCACCTTTTCAGAAATCCTTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTTCT 1586
Db 375 TTGAACGAGGCTCCTTTCAAGATGAAAGAGGAGCACTTGAATCGGCTTAGGCTCTCTCT 316
QY 1587 AAAACCGTGAAGTCCGGAAACGATTTCTCCCGCGCTGTTCCGCACTGCTCCACAGATT 1646
Db 315 AGAAGTGTGCAACTTGGAAACGGTTCTTTCCACGTTGTTCAAGAGTTCTAAATAAAGATC 256
QY 1647 ATCAACTGTGAGGACTTGACTCAACTGCGCTTGGCGGAAGAGACACTGCTGAGAAACGA 1706
Db 255 ATGATGCTGATGATGCTATCTGAGATAGCTTACATGGGAATGATACATAGAAGCGT 196
QY 1707 CTACAAAAGCAAGAGGTACATGGAATACAGAGACACTAAAGAGCGCTTTAGTGTAG 1766
Db 195 CAAGTGAAGAACCAAGGTACATGGAACCTCAAGAAATTTGTCTAAAGCACTTACGGAG 136
QY 1767 GACAATTTGGAATTAGAAATTCGTCCTTCGACAGATTCGACTTCTTCCACATCGAA 1822
Db 135 GATAAAGAAGAAATTTGCTAAGACTAAATCTCTCATCTTGTTCCTCTACATCTAA 80

RESULT 10
LOCUS BG464249 614 bp mRNA linear EST 20-MAR-2001
DEFINITION EML7L1D12.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA sequence.
ACCESSION BG464249
VERSION BG464249.1 GI:13392562
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 614)
AUTHORS Reid, S. P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L. H.
TITLE An EST database from Sorghum: developing embryos
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 610
POLYA=NO.
Location/Qualifiers
1..614
/organism="Sorghum bicolor"
/db_xref="taxon:4558"

Utterback, T., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.

Division

Tel: 1-800-711-6195
 Email: cdna@resgen.com
 For clone info: please contact Resea
 Division tel 1-800-711-6195, email c
 Seg primer: T3.

Division tel 1-800-711-6195, email c
Seq primer: T3.

Location/Qualifiers

1. .700

/cultivar="Kennebec"

```
/db_xref="taxon:4113"
/cclone="cPRO10C3"
```

```
/clone_lib="potato roots"
/clone_lib="potato roots"
```

```

/dev_stage="in vitro grown

```

```
/note="Vector: pBluescript
```

sequencing; The Institute f

Roots were isolated from *in vivo* grown roots were isolated two weeks

cuttings from in vitro grow

8.9%; Score 187.8;

3306; Conservative 0; Mismatches

ACATAAGGCACCTGACTCGGATGATATTGAGTTAGTCTC

ATACAGGCATTGGATTTCAGATGATGTTGAACCTTCTC

E
C
C
E
E
A
C
E
C
C
E
C
E
C
C
E
C
C
E
C
C
C

— — — — —

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

CAC T G T G C T T C A C A T T G C T G C C A T G C G T A A G G A A C C C

AAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGGT

TAAGGGAGCTCATGCATCAGAAATTACATTGGATGGG

ACAAGCCACTATGGCGTTGAATGTAATAATATCCCCG

GGAGGCTGAGTAGGCCTAAGGAGTACCATGC AAAACA

AGGCCGACTATGTGTAGAAATACTAGAGCAAGAAGAC

AGATCGGCTATCTATTGATCTTTTGGACACAGACATG

C
E
*
*
E
*
C
C
C
C
C
E
C
*
C
E
E
E
E
C
C
C
E
C
E
E

SECRET

20100303
CEA 100

KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 667)
REFERENCE van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemiango, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
COMMENT Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.

```

FEATURES
source
    Location/Qualifiers
    1. .667
    /organism="Solanum tuberosum"
    /cultivar="Kennebec"
    /db_xref="taxon:4113"
    /clone="cSTS22E2"
    /clone_lib="cSTS"
    /tissue_type="sprouting eyes from tubers"
    /dev_stage="12-14 weeks post harvest"
    /lab_host="SOLR"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    xhoI; Various sizes of sprouting eyes (2mm to 15mm) were
    taken from tubers. The tubers were incubated at 26C in the
    dark for 2-3 weeks prior to sprouting. The eyes were
    frozen in liquid nitrogen immediately upon removal from
    tubers."
BASE COUNT      197 a    125 c    164 g    181 t
ORIGIN
Query Match      7.8%; Score 163.2; DB 10; Length 667;
Best Local Similarity 57.2%; Pred. No. 4.1e-21;
Matches 316; Conservative 0; Mismatches 233; Indels 3; Gaps 1;

```

QY	896	GAATGTACATAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTGAAAGA	955
Db	16	GAGGATTCTGAAGGCTCTGGAGTCTGATGACATTGACTGCTAACACTACTCCTCGAAGA	75
QY	956	GGATCACACCAATCTAGATGATCGGTGCTCTTCATTTCGCTGTGGCATATTGCAATGT	1015
Db	76	GTCAACGCTCACTTTAAACGATGCTTGCTCTTCATTATGCTGCGCTATTGGCAATC	135
QY	1016	GAGACCGCAACAGACATCTTTTAAACCTTGATCT---TGCCGATGTCAACCATAGGAATCC	1072
Db	136	CAAGGTGTGTGACGAGGTACTTGAGCTGGGTTAGGCGTGATGTCAATCTTCAGAACTC	195
QY	1073	GAGGGGATATACGGTGTCTCATGTGCTGCGATGCGGAGGAGGCCACAAATTGATACTATC	1132
Db	196	CCGAGGATATATGTCCTTCATGTTCGAGCTAGCAAGAGGCCATCAATAATATGGG	255
QY	1133	TCATTGGAAAAGGTGCAAGTGCATCAGAAAGCAACTTTGGAGGTAGAACCGCACTCAT	1192
Db	256	ACTATTGCAAAAGAGCATCGGTCTTTGGATCTACACGGACGCACATACAGCACTATC	315
QY	1193	GATCCGAAACACGCCACTATGGCGGTGTAATGTAATAATATCCCGGAGCAATGCAAGCA	1252
Db	316	CATATGCGCTAGATTGACTCGCTCTAAAGGATTACAATGATCCACGGAGCAAGGAAGGT	375
QY	1253	TTCTCTCAAGCGCGACTATCTGTGAGAAATACTAGACGACGAGACAAACGAGACAAT	1312
Db	376	TACTAATAAGACCGGTTATGCAATTGATGTTTGGAGAGAGATGATTAGGAATCCCTAT	435
QY	1313	TCCTAGAGATGTTCTCCCTCTTTTTCAGTGGCGCGCGATGAATTGAAGATCACGCTGCT	1372
Db	436	GATTGGGAGCATGCTCTTCTTCATCTATTGGTGTGGCTGATGAATTACTCATGAGGTTGCT	495
QY	1373	CGATCTTGAAAATAGAGTTGCATTTGCTCAACGCTCTTTTCCACGGAAGCAAGAGTGC	1432

Db	496	TTTATTGAAATAGATGGGATTGGCAGGATGTTATTCTCCTCAGGAAGCCATGCTAGC	555
Qy	1433	AATGGAGATCGC	1444
Db	556	TATGGAATAGC	567
RESULT	15		
BE493178			
LOCUS			
DEFINITION	BE493178	455 bp mRNA	linear EST 16-APR-2001
ACCESSION	BE493178		Triticum monococcum vegetative apex cDNA library
KEYWORDS	BE493178.1	GI:9659771	Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
SOURCE	EST.		
ORGANISM	Triticum monococcum.		
REFERENCE			
AUTHORS	Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Stamove,B. and Tong,J.C.		
TITLE	The structure and function of the expressed portion of the wheat genomes - Vegetative apex cDNA library from Triticum monococcum Unpublished (2001)		
JOURNAL	Contact: Olin Anderson		
COMMENT	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oanderson@pw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene T3 primer. Location/Qualifiers 1. .455 /organism="Triticum monococcum" /cultivar="DV92" /db_xref="taxon:4568" /clone="WHE0570_C11_F22" /clone_lib="Triticum monococcum vegetative apex cDNA library" /tissue_type="Vegetative shoot apex" /dev_stage="Three weeks-old plants" /lab_host="E. coli XL0LR" /note="Vector: Lambda PBK-CMV (Lambda Zap Express), excised plasmid; Site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised at the University of California, Davis (V. Echenique, B. Stamova , J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."		
BASE COUNT	132 a	94 c	98 g 131 t
ORIGIN			
Query Match	7.6%	Score 160.6;	DB 10; Length 455;
Best Local Similarity	62.8%;	Pred. No. 1.4e-20;	
Matches	272;	Conservative 0;	Mismatches 149; Indels 12; Gaps 1;
Qy	715	TTGCTAATATATGTTGGTAAAGCTTGATGAGCTATTGGATAGATGTAAGAGATTATTG	774
Db	22	TTGCAAACTTATGCAACAATACTTCGCTGAAACTGTTTGAGAGATGCTGGAGATGTTAG	81
Qy	775	TCAAGTCTAATGTAGATATGTTAGTCTTGAAAGTCAATTCGCGAAGAGCTTGTTAAAG	834
Db	82	TCCGGTCAATCTTGACATGATTACTCTTGAGAAGACGATTCCTGGAAGATTGTTATCAAGC	141
Qy	835	AGATAATTGTATGACAGTAAAGAGCTTGTTGGAGGTACCTAAAG	882

```
Db 142 AAATTATTGATTCACGGATAACTCTTGGATTAGCTTACCCGGAAGACAATGGCTGTCTTA 201
QY 883 AGAAACATGCTCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGT 942
Db 202 ACAACACCGTAAGAGGATACCTCAAGGCACCTTGATCTGATGATGGAGCTTGCAGGA 261
QY 943 TGCCTTTTGAAGAGGATCACACCAATCTAGATGATGCTGTCTTTCATTTCGCTGTTG 1002
Db 262 TGCTGCTCACAGAGGCAGACTAACCTTGAATGATGATTTGCATTGCACATGCTGTAG 321
QY 1003 CATATTGCAATGTGAAGCCGCAACAGATCTTTTAAACTTGATCTGCCGATGTCACAC 1062
Db 322 AACACTGTGACTCAAAAATTACACAGAACTTCTGGACATCGCACTTGGGATGTTAATC 381
QY 1063 ATAGGAATCGAGGGATATACGGTGTCTCATGTTGCTCGGATCGGGAAGGAGCCACAA 1122
Db 382 TCAGAAACCCAGAGGTTATACTGTCTTCACATCGCTAGCGGAGAGATCCTAANA 441
QY 1123 TGATACTATCTCT 1135
Db 442 TTGTTGCTCTTCCT 454
```

Search completed: October 8, 2002, 01:20:25
Job time : 1660.95 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 21:30:19 ; Search time 2646.43 Seconds
(without alignments)
17175.023 Million cell updates/sec

Title: US-08-908-884-13
Perfect score: 2172
Sequence: 1 GTGACTTTCTAATGCT.....ATTGAAAAA 2172

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_cm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pi.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_un.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hgt_hum.*
- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgtgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
------------	-------	-------	-------	--------	----	----	-------------

1	578.4	26.6	2104	8	ATU76707	U76707 Arabidopsis
2	578.4	26.6	2154	8	AY050455	AY050455 Arabidopsis
3	576.8	26.6	2011	6	AR087502	AR087502 Sequence
4	576.8	26.6	2011	6	AR087503	AR087503 Sequence
5	549.4	25.3	1597	6	AR087504	AR087504 Sequence
6	527.6	24.3	1668	6	AX351145	AX351145 Sequence
7	517.4	23.8	1608	6	AR087505	AR087505 Sequence
8	513	23.6	1565	6	AX351141	AX351141 Sequence
9	490	22.6	1194	6	AR087506	AR087506 Sequence
10	391.8	18.0	4270	6	AX351127	AX351127 Sequence
c 11	376.4	17.3	140304	8	AP002537	AP002537 Oryza sat
c 12	376.4	17.3	168372	8	AP002746	AP002746 Oryza sat
13	326.8	15.0	5655	8	AR087501	AR087501 Sequence
14	326.8	15.0	5655	8	ATU87794	U87794 Arabidopsis
15	326.8	15.0	96887	8	AC066689	AC066689 Arabidopsis
16	317	14.6	1428	6	AX049426	AX049426 Sequence
17	317	14.6	2368	6	AX049427	AX049427 Sequence
18	316.2	14.6	786	6	AR087507	AR087507 Sequence
19	315.4	14.5	2326	6	AX351139	AX351139 Sequence
20	288	13.3	104738	8	ATF20B18	AL049483 Arabidops
21	288	13.3	196286	8	ATCHRIV64	AL161564 Arabidops
22	287.2	13.2	1830	6	AX049431	AX049431 Sequence
23	287.2	13.2	2120	6	AX049433	AX049433 Sequence
24	283.6	13.1	498	6	AX351135	AX351135 Sequence
25	282.6	13.0	2446	6	AX351143	AX351143 Sequence
26	276	12.7	1824	6	AX049430	AX049430 Sequence
27	276	12.7	2420	6	AX049432	AX049432 Sequence
28	266.2	12.3	2154	6	AX041006	AX041006 Sequence
29	231.4	10.7	2235	6	AX049445	AX049445 Sequence
30	227.2	10.5	1385	6	AX049441	AX049441 Sequence
31	212.2	9.8	705	6	AX049428	AX049428 Sequence
32	202.6	9.3	103785	2	AF003377	AF003377 Oryza sat
33	202.6	9.3	140823	2	AP003371	AP003371 Oryza sat
34	198.4	9.1	706	6	AX049434	AX049434 Sequence
35	185.6	8.5	498	6	AX351133	AX351133 Sequence
36	174	8.0	7789	6	AX041008	AX041008 Sequence
37	173.2	8.0	498	6	AX351137	AX351137 Sequence
38	162.2	7.5	67220	8	AB019224	AB019224 Arabidops
c 39	151.8	7.0	95417	8	ATT16H5	AL024486 Arabidops
c 40	151.8	7.0	197114	8	ATCHRIV51	AL161551 Arabidops
c 41	56.2	2.6	91717	8	AC005662	AC005662 Arabidops
c 42	54.4	2.5	1141	6	AX083744	AX083744 Sequence
43	51.8	2.4	185602	9	AL139081	AL139081 Human DNA
44	50.8	2.3	91303	8	ATF24I3	AL138655 Arabidops
45	49.4	2.3	7218	6	I66494	I66494 Sequence 14

ALIGNMENTS

RESULT 1
ATU76707
LOCUS Arabidopsis thaliana regulatory protein NPR1 (NPR1) mRNA, complete cds.
DEFINITION U76707
ACCESSION U76707.1 GI:1773294
VERSION
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Cao,H., Glazebrook,J., Clarke,J.D., Volko,S. and Dong,X.
TITLE The Arabidopsis NPR1 gene that controls systemic acquired resistance encodes a novel protein containing ankyrin repeats
JOURNAL Cell 88 (1), 57-63 (1997)
MEDLINE 97148688
AUTHORS Cao,H., Glazebrook,J., Clarke,J.D., Volko,S. and Dong,X.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC

FEATURES	Building, Research Dr., Durham, NC 27708-1000, USA	
	Location/Qualifiers	
source	i. .2104	
	/organism="Arabidopsis thaliana"	
	/strain="ecotype Columbia"	
	/db_xref="taxon:3702"	
	/chromosome="1"	
	/map="between GAP-B and m315"	
gene	i. .2104	
	/gene="NPRI"	
CDS	93. .1874	
	/note="ankyrin repeat-containing protein; gene controlling systemic acquired resistance; SAR"	
	/codon_start=1	
	/product="regulatory protein NPRI"	
	/protein_id="AAC49611.1"	
	/db_xref="GI:1773295"	
	/translation="MDTIDGFADSVESISTSFVATDNTDSSIVYLAEEQVLTGPDVS	
	ALQLNSFESVDFSDPDYSDAKLVLDGREVSPHRCVLARSFFKSAALAAKKEK	
	DSNNANVKLEKELAKDYEVDFSVTVLAVVYSSRVPPKGVSECDENCCHVAC	
	RPADFMEIVLYLAFIKPELITLYQRLHLDVVDKVIYEDLVILKLANICGKACMK	
	LDAVKEIVLNSVDMSLEKSLPEELKEIIDRKLEGVKPKVKKHVSINVHKAIDS	
	DDIELVLLKEDHNDACALHFAVAYCNKTAATDLKLDLADVNHNRNPGTYVLH	
	VAMRKPOLIISLLEKASASEATLEGRTALMIAKQATMAVECNINPEQCKHSLVGR	
	LCVLEODKREQLPQVPPSPFAVADELKMTLIDLENVALQRLKPTPEAQAMEI	
	AEWKGTCEPIVTSLEPDRLTGKRTSPGVKIAPPRILEEHOSRLKALSKTVELGKRF	
	PRCSAVLDQINCEDLTOLACGEDDTAEKRLQKQRYWEIQETLKKAFSEDNLELGS	
	SLTDSISSTKSTGSKRNRKLSHRRR"	
BASE COUNT	606 a	431 c 482 g 585 t
ORIGIN		
Query Match	26.6%;	Score 578.4; DB 8; Length 2104;
Best Local Similarity	62.8%;	Pred. No. 3.7e-138;
Matches 982;	Conservative	0; Mismatches 546; Indels 36; Gaps 4;
Qy	415	CGGAGTTTGACTACTTGGCGGACGCTAAGCTTGTGTGTTCCGGCCCGGTGAAGGAAATTC 474
Db	268	CGCGGATGATTTCTACAGCGAGCTTAAGCTTGTCTCTCCGAC---GGCCGGGAAGTTT 324
Qy	475	CGGTGCACCGGTGCATTTCTCGCGGAGGATCGGTCTTTAAGAATTTGTTCTCGCGTA 534
Db	325	CTTTCCACCGGTGGTTTGTACGCGAGAAGCTCTTTCTTCAAGAGCGCTTTAGCCGCG 384
Qy	535	AAAAGGAGAAGATAGTAGT-----AAGGTGGAATGAAGGAGGTGA 576
Db	385	CTAAGAGGAGAGAGACTCCAACAACCCGCGGTGAAGCTCGAGCTTAAGGAGATTG 444
Qy	577	TGAAAGAGCAGGTGAGCTGATGATGCTGAATGAGTGTATTGGCTTATTGTATATAG 636
Db	445	CCAAGGATTACGAATCGGTTTCGATTCGGTTGTGACTGTTTGGCTTATGTTTACAGCA 504
Qy	637	GTAAGTTAGCCCTTACCTTAAGATGTGTGTTGTGTGGACAATGACTGCTCTCATG 696
Db	505	GCAGAGTGAGACCCGCCCTTAAAGAGGTTTCTGAATGCGCAGCAGAGAATGTGCGCAC 564
Qy	697	TGGCTTGTAGCCAGCTGTGCAATCTCGTTGAGCTTTTGTACACATCATATTTACCTTC 756
Db	565	TGGCTTGGCCGCGCGGTGATTTTCATGTTGGAGGTCTCTATTGGCTTTTCATCTTCA 624
Qy	757	AGATCTCTGAATTTGGTTGACAAGTTTCAGACACACCTACTGGATATTTCTTGACAAA 816
Db	625	AGATCCCTGAAATTAATTAATCTCTATCAGAGGCACTTATTGGACGTTGTAGACAAA 684
Qy	817	CAGCAGAGCAGTGAATGATGTTTATCTGTGCAACAATTTGTGGTAAAGCATGCGAGA 876
Db	685	TTATAGAGGACACATTTGGTTATACTCAAGCTTGCTAATATATGTGGTAAAGCTGTATGA 744
Qy	877	GATTGCTTCAAGCTGCAATTAATTTGTCAAGTCTAATGTTGATPATCATACCCCTTG 936
Db	745	AGCTATTGGATAGATGTAAGAGATTAATTTGCAAGTCTAATGTAGATATGTTAGTCTTG 804
Qy	937	ATAAGCCTTCGCTCATGACATTTGTAACAAATTAATTAATTAATTAATTAATTAATTA 996

RESULT 2

QY	1297	GACCTTCTGATCTGACATCCGATCGAAGAAAGACACTTCAAAATGCCAAGAGGCTCACTA	1356
Db	1219	GTGCATCAGAAGCACTTTGGAGGTAGAACCGCACTCATGATCGCAAAACNAGCCACTA	1278
QY	1357	GGCTTGTGGATTTCAGTAAGTCTCCGGAGGAAGGAAATCTGCTTCGAATGATCGGTTAT	1416
Db	1279	TGCGGTTGAATGTAATAATATCCGGAGCAATGCAAGCATTTCTCAAAAGCCGACTAT	1338
QY	1417	GCATTGAGATTCTGGAGCAAGCAGAAAGAGAGACCCCTGCTAGAGAGGCTTCTGTAT	1476
Db	1339	GTGTAGAAATACTAGACGAAGAAGCAAAACGAGAACAAATTCCTAGAGATGTTCTCCCT	1398
QY	1477	CTCTTCTGATGGCAGCGATGATTTTCGCTATGAAGCTGTTATACCTTGAATAAGATGTTG	1536
Db	1399	CTTTTCAGTGGCGCGGATGAAATGAAATGACGCTGCTCGATCTTGAANATAGATG	1458
QY	1537	GCCTGGCTAAACTCTCTTTTCCAAATGGAAGCTAAAGTTGCAATGGACATGCTCAAGTTG	1596
Db	1459	CACCTGCTCAACGCTCTTTTCCAAACGGAAGCACAAAGCTGCAATGGAGATCGCGAAATGA	1518
QY	1597	ATGGCACTCTGAGTTCCCACTGGCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA	1653
Db	1519	AGGGAACATGTGAGTTTCATAGTACTAGGCTCGAGGCTGACCGCTCFACCTGGTACGAAGA	1578
QY	1654	GGACAACAGTAGATTTGAACGAGGCTCTCTTCAAGATAAAGAGGAGCACTTGAATCGGC	1713
Db	1579	GACATCACCGGCTGTAAAGATAGACCTTTCAGATCTCAGAGAGCATCAAGATAGAC	1638
QY	1714	TTAGAGCACTCTCAGAACCTGTAGAATCTGGAAAACGCTTCTTCCACGTTGTTCAAGAG	1773
Db	1639	TAAAAGCGCTTTTAAACCGTGGAACTCGGGAACGATTTCTCCGCGCTGTTCGGCAG	1698
QY	1774	TTCTAATATAGATCATGGATGCTGTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATA	1833
Db	1699	TGCTCGACAGATATGAAGTGTGAGACTTTGACTCAACTGGCTTCGGGAGAGACGACA	1758
QY	1834	CGGCAGAAAGCGCTCAACTGAAGAAGCAAGGTACATGGAACCTTCAAGAAATTTCTGACTA	1893
Db	1759	CTGCTGAGAAACGACTACAAAAGCAAGAGTACATGGAAATACAAAGACACACTAAAGA	1818
QY	1894	AAGCAATCTAGGAGTAAGAAGATATATGATAAGACTACACACATCTCCTCATCTTGT	1953
Db	1819	AGGCTTTAGTGAGGACAATTTGGAATTTAGGAATTCGTCCCTGACAGATTTGACTTCTT	1878
QY	1954	CCTC 1957	
Db	1879	CCAC 1882	

RESULT 3	AR087502	2011 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AR087502	Sequence 6 from patent US 5986082.			
DEFINITION	AR087502				
ACCESSION	AR087502.1	GI:10014265			
VERSION	AR087502.1				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2011)				
AUTHORS	Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.				
TITLE	Altered forms of the NIM1 gene conferring disease resistance in plants				
JOURNAL	Patent: US 5986082-A 6 16-NOV-1999;				
FEATURES	Location/Qualifiers				
BASE COUNT	563 a 472 c 472 g 559 t				
ORIGIN	1..2011				
	/organism="unknown"				
Query Match	26.68;	Score	576.8;	DB 6;	Length 2011;
Best Local Similarity	62.7%;	Pred.	No. 9.7e-138;		

Matches	981;	Conservative	0;	Mismatches	547;	Indels	36;	Gaps	4;
QY	415	CGGAGTTTGTACTTCCGCGACGCTAAGCTTGTGGTTTCCGGCCCGGTGTAAGGAATTC	474						
Db	218	CGCCGATGATTTCTACAGCGACGCTAAGCTTGTCTCTCCGAC---GGCCGGAAGTTT	274						
QY	475	CGGTGCACCGGTGCATTTTGTCCGCGAGGAGTCGGTTCCTTTAAGAAATTTCTCTCGGTA	534						
Db	275	CTTTCCACCGGTGGCTTTTGTACGCGAAGACTCTTTCTTCAAGAGCGCTTTAGCCCGCG	334						
QY	535	AAAAGGAGAAGATAGTAGT-----AAGGTGGAATTTGAAGAGAGGTGA	576						
Db	335	CTAAGAAGGAGAAAGACTCCACAAACACCCGCCCGCTGAAGCTCGAGCTTAAGGAGATTG	394						
QY	577	TGAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTTGTAATAGT	636						
Db	395	CCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGACTGTTTGGCTTATGTTTACAGCA	454						
QY	637	GTAAGTTTAGCCCTTACCTTAAGATGTGCTGTTTGTGGCAATGACTGCTCTCATG	696						
Db	455	GCAGAGTGAGACCCCGCCTAAAGGAGTTTCTGAATGGCAGACGAGAAATGCTGCCACG	514						
QY	697	TGGCTTGPAGCCAGCTGTGGCATTCTCTGTTGAGGTTTGTACACATCATTTTACCTTTC	756						
Db	515	TGGCTTGGCCGCCGCGGTGATTTTCATGTTGGAGGTTCTCTATTGGCTTTCATCTTCA	574						
QY	757	AGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTACTGCGATTTCTTGACAAAAC	816						
Db	575	AGATCCCTGAATTAATTACTCTCTATCAGAGGCACCTTATTGGAGCTTTGTAGACAAG	634						
QY	817	CAGCAGCATGTAAATGATGCTTTTATCTGTTGCAACATTTGTGTAAGCATGCGAGA	876						
Db	635	TTATAGAGGACACATTTGGTTATCTCAAGCTTGCTTAATATATGTTGGTAAAGCTTGT	694						
QY	877	GATTGCTTCAAGCTGCTATGAGATTATTGTCAAGTCTTAATGTTGATATCATACCCCTG	936						
Db	695	ACCTATTGGATAGATGTAAGAGATTATTGTCAAGTCTAATGATAGATGTTAGTCTTG	754						
QY	937	ATPAAAGCCTTGCCCTCATGACATTTGTAACAATAATCTAGTATTCAGGCGGAACCTGG	996						
Db	755	AAAAGTCATTGCGGGAAGAGCTTTGTTAAAGAGATAAATGTAGACGTAAGAGCTTGG	814						
QY	997	TACAAGGCGCTGAAAGCAACGCTTTTCCTGATAAACATGTTAAGAGGATACATAGGCG	1056						
Db	815	TGGAGGTACCTTAAAGTAA-----AGAAACATGCTCTGNAATGTACATAGGCAC	862						
QY	1057	TGGATTCTGATGATGTTGAATTTACTACAATTTGCTTAAGAGAGGGGCATACTACCC	1116						
Db	863	TTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTCAAAAGAGGATCACACCAAT	922						
QY	1117	ATGATGCATATGCTCTCCATTAAGCTGTAGCGTATTGGATGTCAAAGACTACACAGAC	1176						
Db	923	ATGATGCGGTGCTCTTCAATTTTCGCTTTCGCTATATTGCAATGTGAAGACCCGACAG	982						
QY	1177	TTCTAGATCTTCCACTTCTGATATTAAATCATCAAAAATTTCAAGGGGATACAGGTG	1236						
Db	983	TTTTAAACCTTGTCTTCCGATGTCACCATAGGAATCCGAGGGGATATACGGTGTTC	1042						
QY	1237	ATGTTGACGCCATGAGGAAGAGCCTTAAATTTGTAGTGTCCCTTTTAAACCAAGAGG	1296						
Db	1043	ATGTTGCTCGATGCGAAGAGGAGCCACAAATTTGATATCTATCTATTGGAAGAGG	1102						
QY	1297	GACCTTCTGATCTGACATCCGATGGAAGAAAAGCACTTCAATCCCAAGAGGCTCACTA	1356						
Db	1103	GTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCCTCATGATCGCAAAACNAGCCACT	1162						
QY	1357	GGCTTGTGATTTTCAGTAAAGTCTCCGAGGAAGGAAATCTGCTTCGAATGATCGGTTAT	1416						
Db	1163	TGGCGTTTGAATGTAATAATATCCCGGAGCAATGCAAGCAATTTCTCAAGGCCACTAT	1222						
QY	1417	GCATTGAGATTTGGAGCAAGCAGAAAGAGACCCCTCTGCTAGGAGAGCTTCTGTAT	1476						
Db	1223	GTGTAGAAATACTAGACGAAGAAGACAAACGAGAGACAAATTCCTAGAGATGTTCTCT	1282						

QY	1654	GGACACAGTAGATTTGAAACGAGGCTCCTTTCAAGATAAAAGAGGACGACCTTGAATCGGC	1713		
Db	1463	GAACATCACCGGTGTAAGATAGCACCTTTCAAGATCTTAGAAGACATCAAAAGTAGAC	1522		
QY	1714	TTAGAGCACTCTCTAGAACCTGTAGAACTTGGAACGCTTCTTTCCACGTTGTTTCAGAAG	1773		
Db	1523	TAAAGCGCTTTCTTAAACCGTGGAACTCGGGAACGATTCTTCCCGCGCTGTTTCGGCAG	1582		
QY	1774	TTCTAAATAAGATCATGATGCTGATGACTTGTCTGAGATAGCTTACATGGGAATGATA	1833		
Db	1583	TGCTCGACAGATTATGAACCTGTGAGGACTTGACTCAACTGGCTTGGCGAGAGACACACA	1642		
QY	1834	CGCGAAGAGCGCTCAACTGAAGAAGCAAAAGGTACATGGAACCTTCAAGAAATTTCTGACTA	1893		
Db	1643	CTGCTGAGAAAGCACTACAAAAGAAAGCAAAAGGTACATGGAATACAAAGAGACACATAAGA	1702		
QY	1894	AAGCAATTCACGTGAGGATAAAGAAGAATATGATAAGACTTAACAACATCTCCTCATCTTGT	1953		
Db	1703	AGGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTTGTCCCTGACAGATTTCGACTTCTT	1762		
QY	1954	CCTC 1957			
Db	1763	CCAC 1766			
RESULT 5					
AR087504					
LOCUS	AR087504	1597 bp	DNA linear PAT 07-SEP-2000		
DEFINITION	Sequence 9 from patent US 5986082.				
ACCESSION	AR087504				
VERSION	AR087504.1 GI:10014267				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	Uknes,S.Joseph, Hunt,M.Denise, Steiner,H. and Ryals,J.Andrew.				
TITLE	Altered forms of the NIM1 gene conferring disease resistance in plants				
JOURNAL	Patent: US 5986082-A 9 16-NOV-1999;				
FEATURES	Location/Qualifiers				
source	1..1597				
BASE COUNT	467 a	304 c	381 g 445 t		
ORIGIN	/organism="unknown"				
Query Match 25.3%; Score 549.4; DB 6; Length 1597;					
Best Local Similarity 63.9%; Pred. No.1.le-130;					
Matches 870; Conservative 0; Mismatches 476; Indels 15; Gaps 2;					
QY	600	GATGCTGTAATCAGTGTATTGGCTTATTGTTATAGTGGTAAAGTTAGGCGCTTCACCTAAA	659		
Db	4	GATTGCGTTGTGACGTGTTTGGCTTATGTTTACACGACGAGTGAGACCGCGCTTAAA	63		
QY	660	GATGTGTGTGTTTGTGTGGCAATGACTGCTCTCATGTGGCTGTAGGCGAGCTGTGGCA	719		
Db	64	GGAGTTTCTGAATGCGCAGACGAGAATTCGTCGCCACGTGGCTTGCGCGCGCGGTGGAT	123		
QY	720	TTCTCGTTGAGGTTTGTGTACACATCATTTACCTTTTCAGATCTCTGAAATTTGTTGACAAG	779		
Db	124	TTTCATGTTGGAGGTGCTCTATTGTTGGCTTTCATCTTCAAGATCCCTGAAATTAATTAATCTC	183		
QY	780	TTTCAGAGACACCTACTGGATATTCTTGACAAAACCTGCGACGACGATGTAATGATGTT	839		
Db	184	TATCAGAGCACTTATGTGACCTTGTAGACAAAGTTGTTATAGAGGACACATTTGGTTATA	243		
QY	840	TTATCTGTGCAAAATTTGTGGTAAAGCATCGGAGAGATTGCTTTCAAGCTGCATTGAG	899		
Db	244	CTCAAGCTTGCTAATATATGTGTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAG	303		
QY	900	ATTATTGTCAAGTCTAATCTGTATATCATAAACCTTGTATAAAGCCTTGGCTCATGACATT	959		

Db	304	ATTATTGTCAAGTCTAATGTAGATATGGTTAGTCTTGTAAGAACTCATTTGCCGGAAGAGCTT	363
QY	960	GTAACAAATTTACTGATTCACGAGCGGAACCTTGCTGTACAAAGGCGCTGAAAGCAACGGT	1019
Db	364	GTTAAAGACATAATTGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAA-----	418
QY	1020	TTTCTGTATAACACATGTTAAGAGGATACATAGGGCATTTGGATTCTGTAGTATGTTGAATTA	1079
Db	419	-----AGAAACATGCTCGAATGTACATAAGGCATTTGACTCGGATGATATTAGTTA	471
QY	1080	CTACAAATGTTGCTTAGAGAGGGGCATCTACCTAGATGATGCATATGCTCTCCATTAT	1139
Db	472	GTCAAGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCGGTGCTCTTCATTTC	531
QY	1140	GCTGTAGCGTATTGCGATGCAAGACTACAGCAGAACTTCTTAGATCTTGCACCTTGCAT	1199
Db	532	GCTGTTGCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTGCAGAT	591
QY	1200	ATTAATCATCAAAATTTCAAGGGGATACAGGTGCTGCATGTTGCGCCATGAGGAAGAG	1259
Db	592	GTCAACCATAGGAATCCGAGGGGATATAGGTGCTTTCATGTTGCTGCGATGCGGAAGAG	651
QY	1260	CCTAAAATTTAGTGTCCCTTTTAAACCAAGGAGCTAGACCTTCTGATCTGACATCCGAT	1319
Db	652	CCACAATTTGATATCTCTATTGGAAAGGTGCAAGTGCATCAGAACCACTTTGGAA	711
QY	1320	GGAAGAAAGCACTTCAAAATCGCCAAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCT	1379
Db	712	GTTAGAACCCCACTCATGATCGCAAAACAGCCACTATGCGGTTTGAATGTAATAATATC	771
QY	1380	CCGGAGGAAGAAATTCGTTTCGAATGATCGGTTTATGCAATTCAGATTCTGGAGCAAGCA	1439
Db	772	CCGGAGCAATGCAAGCATTTCTCTCAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAA	831
QY	1440	GAAAGAGAGACCCCTCTGCTAGGAGAGCTTCTGTATCTTCTGCTATGGCAGCGATGAT	1499
Db	832	GACAAAGCAAGAAATTCCTAGAGATGTTCTCCCTCTCTTTGCACTGGCGCCGATGAA	891
QY	1500	TTGCGTATGAAGCTGTTTATACCTTGAAATPAGATTGTGGCTGGCTAAACTTCCTTTTCCA	1559
Db	892	TTGAAGATGACGCTGCTCGATCTTGAAATPAGATTGTGCACTTCTCAAGCTCTCTTTTCCA	951
QY	1560	ATGGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTGATGGCACTTCTGAGTTCCCACTG	1619
Db	952	ACGGAAGCACAGCTGCAATGGAGATCGCGCAATGAAGGAACATGTGAGTTTCATAGTG	1011
QY	1620	GCTAGCATCG---GCAAAAAGATGGCTTAATGCACAGAGGACACAGTAGATTTTGAACGAG	1676
Db	1012	ACTAGCCTCGAGCCTGACCGCTCTCACTGGTACGAGAGAAACATCACCGGCTGTAAAGATA	1071
QY	1677	GCTCCTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGACACTCTCTAGAACTGTA	1736
Db	1072	GCACCTTTCAGATCTCTAGAGAGCATCAAAAGTAGACTAAAGAGCGCTTTCTTAAACCGTG	1131
QY	1737	GAACTTGGAAAAGCTTCTTTCCACGTTGTTTCAAGAGTTCTTAAATAGATCATGGATGCT	1796
Db	1132	GAACTCGGAAACATTTCTTCCCGCGCTGTTCGGCAGTGTCTCGACAGATTTAGAACTGT	1191
QY	1797	GATGACTTGTCTGAGATPAGTTTACATGGGGAATGATACGGCAGAGAGCGCTCAACTGAAG	1856
Db	1192	GAGGACTTGTCACTCAACTGGCTTGGCGAGAGAGACACTGCTGAGAAACGACTACAAAAG	1251
QY	1857	AAGCAAGGTACATGGAACTTTCAGAAATTTCTGACTAAAGCATTTCACTGAGGATAAGAA	1916
Db	1252	AAGCAAGGTACATGGAAATTCAGAGACACTAAAGAGGCGCTTTAGTGAGGACAAATTTG	1311
QY	1917	GAATATGATAAGACTAAACAACATCTCCTCATCTTCTTGTTCCTC	1957
Db	1312	GAATTAGAAATTTGTCCCTGACAGATTTCGACTTCTTCCAC	1352
RESULT 6			
AX351145			

Db	947	CTAAATCGTTGCTCTCCCTTTTAAACCAAGGTCGCCGGCTTCAGATTTTACATTTGATG	1006
Qy	1321	GAAGAAAGCACTTCAAATCCCAAGAGAGGCTCACTAGGCTTGTGGATTTCAAGTAAGTCTC	1380
Db	1007		
Qy	1381	CGAGGAAGGAAATCTGCTTCGAATGATCGGTTATATGCATTGAGATTTCTGGAGCAAGCAG	1440
Db	1067	CTGAGAAGGAAGCGCTCCCAATGATAAATATGCAATGAGATATGAGCAAGCTG	1126
Qy	1441	AAAGAAGAGACCCCTCTGCTAGGAGAAGCTTCGTATCTTCTGCTATGGCAGCGCATGATT	1500
Db	1127		
Qy	1501	TGCGTATGAGCTGTTATACCTTGAATAGAGTTGGCTGGCTGCTAACTCCTTTTCCAA	1560
Db	1187	TTCTGTGGAAGTTACTGTACCTTGAACACCGAGTTGCTTTGGCAAGGATAATGTTTCCAA	1246
Qy	1561	TGGAAGCTAAAGTTGCAATGGACATTCGCTCAAGTTGATGGCACTTCTCAGTTCCCACTGG	1620
Db	1247	TTGAGGCAAGAGTAGCAATGGACATTCGCTCAAGTGGATGGTACTTTGGAATTTACCTTG	1306
Qy	1621	CTAGCATCGGCAAAAGATGGCTAATGCAGAGAGGACAACAGTAGATTTGAACGAGGCTC	1680
Db	1307	GT-----TCTAGTACAATCCACTCTGGAGATAACAACGGTTGATCTGAATGATACTT	1360
Qy	1681	CTTTCAAGATAAAGAGAGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTCTAGAAC	1740
Db	1361		
Qy	1741	TTGAAAAACGCTTCCTTCCAGGTGTTTTCAGAAAGTTCTAAATAAGATCATCGATGCTGATG	1800
Db	1421	TCGGCAACGTTTCTTCCACGCTGTTTCAATTCGCTGACAAGATCATGACCATGA--	1478
Qy	1801	ACTGCTCGAGATAGCTTACATGGGGAATGATACGGCAAGAGAGCGTCAACTGAAGAAGC	1860
Db	1479	----ACCTGAGCTGGCTTCCCTCGAAGAGATGCATCTCCGA-----GAGGAAGA	1525
Qy	1861	AAAGTATACGAACTTCAAGAAATTCGACTAAGCAATTCACAGATTCACGATAAAGCAAT	1920
Db	1526	GGAGTTTTCAGCACTGCAAGATACGCTTTCGAAGCGCTTCAGGAGGACAAGGAGGT	1585
Qy	1921	ATGATAAGCACTAACAACTCTCCTCATCTTCTTCTACATCTTAAGGAGATAGATAA	1978
Db	1586	TTACAGAAACACAACCCCTTCATCTTCGTATCTCGACGTCCTACAGTACACAGGAA	1643
RESULT 7			
AR087505			
LOCUS	AR087505	1608 bp	DNA linear PAT 07-SEP-2000
DEFINITION	Sequence 11 from patent US 5986082.		
ACCESSION	AR087505		
VERSION	AR087505.1	GI:10014268	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1608)		
AUTHORS	Uknes,S.Joseph., Hunt,M.Denise., Steiner,H.-Y. and Ryals,J.Andrew.		
TITLE	Altered forms of the NIM1 gene conferring disease resistance in plants		
JOURNAL	Patent: US 5986082-A 11 16-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..1608		
BASE COUNT	447 a 340 c 385 g	436 t	
ORIGIN	/organism="unknown"		
Query Match	23.88;	Score 517.4;	DB 6; Length 1608;
Best Local Similarity	63.04;	Pred. No. 2e-122;	
Matches	882; Conservative	0; Mismatches 481;	Indels 36; Gaps 4;
Qy	415	CGAGTTTGACTACTTCGCCGACGCTAAGCTTGTTGGTTTCCGGCCGCTGTAAGCAATTC	474

```

Db 218 CGCGGATGATTTCTACAGGAGCCTAAGCTGTCTCTCCGAC-----GCCCGGAAGTTT 274
QY 475 CGGTGCACCGGTCATTTTGTGCGGAGGAGTCGGTCTTTTAAAGAAATTTGTTCTCGGGTA 534
Db 275 CTTTCCACCGGTGCGTTTGTGTCAGCGAAGAGCTCTTTCTTCAAGAGCGCTTTAGCGCGG 334
QY 535 AARAGGAGAAGATAGTAGT-----AAGGTGGAATGAAGGAGGTGA 576
Db 335 CTAAAGAGGAGAAGAGACTCCAAACACCGCCCGCTGAAGCTCGAGCTTAAGGAGATTG 394
QY 577 TGAAGAGCATGAGGTGAGCTATGATGCTGTATATGAGTGTATTGGCTTATTGTATAGTG 636
Db 395 CCRAGGATTACGAAGTCGGTTTCGATTGCTGTGACTGTTTGGCTTATGTTTACAGCA 454
QY 637 GTAAAGTTAGCCCTTCACCTAAAGATGTGTGTTTGTGTGGACATGACTGCTCTCATG 596
Db 455 GCAGAGTGAGACCGCGCCCTAAAGGAGTTTCTGAATGCGCAGACGAGAATTGCTGCCACG 514
QY 697 TGGCTTGTAGCCAGCTGTGGCATTCCTGTTGAGGTTTGTGATACATCATTTACCTTTC 756
Db 515 TGGCTTCCCGCGCGGTGGATTTCAATGTTGGAGGTTCTATTTGGCTTTCATCTTCA 574
QY 757 AGATCTCTGAATTTGGTTGACAAGTTTTCAGAGACACCTACTGGATATTTCTTGACAAAAGT 816
Db 575 AGATCCCTGAATTAATTAATCTCTATCAGAGGCACATTATTGGACGTTGTAGACAAAAGTTG 634
QY 817 CAGCAGAGCATGTAATGATGGTTTTATCTGCTTCAACATTTGTGTGAAGCATGCGAGA 876
Db 635 TTATAGAGGACACATTTGCTTACTCAAGCTTGCTAATATATGTTGTAAGCTTGTATGA 694
QY 877 GATTGCTTTCAAGCTGATTTGAGATTTTCAAGTCTAATGTTGATATCATAAACCTTTG 936
Db 695 AGCTATTGGATAGATTGAAGACATTTATGCTCAAGTCTAATGTAGATATGGTTAGTCTTG 754
QY 937 ATAAAGCCTTGCCTTCATGACATTTAAACAAATTAATGATTCAACGCGGGAACCTTGGTC 996
Db 755 AAAAGTCATTTCCGGAAGAGCTTGTAAAGAGATAATTTGATAGACCTAAAGAGCTTGGTT 814
QY 997 TACAAGGCGCTGAAGCAACCGTTTTCTCTGATAAAGCTGTAAGAGGATACATAGGCGAT 1056
Db 815 TGGAGGTACCTAAAGTAA-----AGAACATGCTCTCAATGTACATAAAGGCAC 862
QY 1057 TGGATTCGTATGATGTTGAATTAATCAAAATGTTGCTAAGAGAGGGGCATPACCCCTAG 1116
Db 863 TTGACTCGGATGATTTAGTGTAGTCAAGTTGCTTTTGAAGAGGATACACCAATCTAG 922
QY 1117 ATGATGATATGCTCTCCATATGCTGTAGCGTATTCGGATGCAAGACTACAGCAGAAC 1176
Db 923 ATGATGCGTGTGCTTTTCATTTGCTGCTGTTGCAATTTGCAATGTGAAGCCGCAACAGATC 982
QY 1177 TTCTAGATCTTGCACTTTGCTGATTAATCATCAAAATTCAGAGGGGATACACGGTGTGC 1236
Db 983 TTTTAAACTTTGATCTTCCGATGCTCAACCATAGGATCCGAGGGATATACGGTGTTC 1042
QY 1237 ATGTTGAGCAGCATGAGAAAGAGCCTAAATTTGATGTGCCCTTTTAAACCAAGAGAGCTA 1296
Db 1043 ATGTTGTGCGATGCGGAAGGACCAATTTGATCTATCTCTATTGTTGAAAAGAGTGCAA 1102
QY 1297 GACCTTCTGATCTCACATCCGATGGAAGAAAGACACTTCAAAATCCGCAAGAGGCTCACTA 1356
Db 1103 GTGCATCAGAAGCAACTTTTGAAGGTGAACCGCCTCATGATGCGCAAAACAGCCACTA 1162
QY 1357 GGCTTTGTGATTTTCAGTAAGTCTCCGAGGAAGGAAATCTGCTTCGAATGATCGGTTAT 1416
Db 1163 TGGCGGTTGATGTAATTAATATCCCGAGCAATGCAAGCATTTCTCTCAAAGGCGGACTAT 1222
QY 1417 CATTGAGATTTCTGGAGCAAGCAGAAAGAGACCCCTCTGCTAGGAGAGCTTCTGTAT 1476
Db 1223 GTGTAGAAATTAAGCAGAAAGCAACGAGCAAAATTCCTAGAGATGTTCCCTCCCT 1282
QY 1477 CTCCTTGTATGCGAGGCGATGATTTGCTATGAAGCTGTTATACCTTGTAAATAGAGTTG 1536

```

```

Db 1283 CTTTTGCAGTGGCGCCGATGAATTTGAAGATAGCGCTGCTCGATCTTTGAAAATAGAGTTG 1342
QY 1537 GCCTGGCTAAACTCCTTTTCCCAATGGAAGCTAAAGTTGCAATGACATTCCTCAAGTTG 1596
Db 1343 CACTTGTCTCAACGCTCTTTTCCACGGAAGCAAGCTGCAATGAGATGCGCGAATGA 1402
QY 1597 ATGGCAGCTTCTGAGTTCACACTGGCTAGCATCG---GCAAAAAGATGGCTTAATCACAGA 1653
Db 1403 AGGGAACATGTGAGTTCATAGTACTAGCTCGACCTCGACCTGCTCCTGCTACGAAGA 1462
QY 1654 GGACAACAGTATGATTTGAACAGGCTCCTTTCAAGATATAAAGAGAGGACACTTGAATCGGC 1713
Db 1463 GAACATCACCGGGTGTAAAGATAGCACCTTTTCAGAACTCTAGAAGAGCATCAAAAGTAGAC 1522
QY 1714 TTAGAGCACTCTCTAGAAGCTGTAGAAGCTTGAAAAACGCTTCTTCCAGCTTGTTCAGAAG 1773
Db 1523 TAAAGCCCTTCTTAAACCGTGGNACTCGGAAACGATTTCTCCCGGCTGTTTCGGCAG 1582
QY 1774 TTCTAAATAAGATCATGGA 1792
Db 1583 TGCTCGACACAGATTATGAA 1601

RESULT 8
AX351141
LOCUS AX351141 1565 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 15 from Patent WO0166755.
ACCESSION AX351141
VERSION AX351141.1 GI:18616494
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (sites)
Wang, H.X., Salmeron, J.M., Willits, M.G. and Lawton, K.A.
Monocotyledonous plant genes and uses thereof
Patent: WO 0166755-A 15 13-SEP-2001;
Syngenta Participations AG (CH)
FEATURES
source
1..1565
/organism="Oryza sativa"
/db_xref="taxon:4530"
<!.1263
/feature="unnamed protein product"
/codon_start=1
/protein_id="CAD22846.1"
/db_xref="GI:18616495"
/translation="CAPPPARAGGLLLLLLAELTNLFORRLDVLDDKVEVDNLLLL
SVANLCNKSCKMLERCLDMVVRNLDNMTLEKSLPDIKQIDARLSGLISPENK
GFPNKHVRIHRALEDSDVELVRLMTEGOTNLDDAFALHYAVEHCDKSKITTELLDLA
LADYNHRNPGTYVLIHAARREPKIIVSLTKGARPDYFDGRKAVQISKRLTKOG
DYFVHTREGKPKDRLCIELEQARRDPOLGEASVSLAMAGESRLRGLLYLENRYA
LARIMFMEARVANDIAQVDCGTLEFLNGSGANPPPPORTVDLNEPFTMKESHAR
MTALSKTVELGKREFPRCSNVLDKIMDDETDPVSLGRDTSNAEKRRKRFHLDVLQKAF
HEDKEENDRSLSSSSSTSGAIPRR"
BASE COUNT 451 a 346 c 367 g 401 t
ORIGIN

Query Match 23.6%; Score 513; DB 6; Length 1565;
Best Local Similarity 65.7%; Pred. No. 2,7e-121;
Matches 785; Conservative 0; Mismatches 395; Indels 15; Gaps 2;

QY 760 TCTCTGAATTTGGTTGACAAAGTTTCAGAGACACCTACTCGATATTTTCGACAAAACCTCGAG 819
Db 50 TCGCGGAGCTCACCAACCTTTCCAGCGCGCTCTCTGATGCTCTGTTGATAAGTTGAAG 109
QY 820 CAGACGATGATGATGTTTATCTGTGCAACATTTGTGTAAGCATTTGTGTAAGCATGCGAGAGAT 879
Db 110 TAGATAACCTCTTATGATCTTCTGTGCGCAACTTATGCAACAAATCTTCATGATGAAC 169
QY 880 TGCTTTCAAGCTGATGATGATTTATGTCAGCTCTAATGTTGATATCATACACCTTGTATA 939

```


Db	712	GGTAGACCGCACTCATGATCGAAACAACCCACTATGCGGGTGAATGTAATAATATC	771
Qy	1380	CCGGAGGAAGAAATCTGCTCGAATCGGTTATGCAATGTAGATCTGGGCAAGCA	1439
Db	772	CCGGAGCAATGCAAGCATCTCTCAAGGCGGACTATGTGTAGAAATACTAGACAAAGAA	831
Qy	1440	GAAGAAGACAGCCCTCTGCTAGGAGAAAGCTCTGTATCTCTGTATGTCATGGCAGGCGATGAT	1499
Db	832	GACAACGAGAACAAATTCCTAGAGATGTTCTCCCTCTTTTGGAGTGGCGCGATGAA	891
Qy	1500	TTCGATTAAGAGCTTTTATACCTTGAAATAGAGTTGGCCCTGGCTAAACCTCTTTTCCA	1559
Db	892	TTGAGATGACGCTGCTCGATCTTGAAATAGAGTTGCACTGTCTCAAGCTCTTTTCCA	951
Qy	1560	ATGGAAGTAAGTTGCAATGGACATCTCTCAAGTTGATGGCACTTCTGAGTTCCTCCACTG	1619
Db	952	ACGGAAGCACAAAGCTGCAATGGATGCCGGAATGAAGGAACATGTGTGATTCATAGTG	1011
Qy	1620	GCTAGCATCG---GCAAAAAGATGGCTAATGCACAGAGGACACAGTAGATTTTGAACGAG	1676
Db	1012	ACTAGCCTCGAGCGCTGACCGTCTACTGGTAGAGAGAACATCACCGGTGTAAAGATA	1071
Qy	1677	GCTCCTTTCAAGATAAAGAGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTGTA	1736
Db	1072	GCACCTTTTCAAGATCCTAGAAGACATCAAAAGTAGACTAAAAGGCGCTTCTTAAACCGTG	1131
Qy	1737	GAACCTTGAAACGCTTCTTCCAGTTGTTTCAGAAAGTTCTTAATAGATCATGGA	1792
Db	1132	GAACTCGGGAACGATTTCTCCGCGCTGTTCCGGCAGTGCTCGACCAAGATTATGAA	1187
RESULT 10			
AX351127			
LOCUS	AX351127	4270 bp	DNA linear PAT 06-FEB-2002
DEFINITION	Sequence 1 from Patent WO0166755.		
ACCESSION	AX351127		
VERSION	AX351127.1	GI:18616481	
KEYWORDS	bread wheat.		
SOURCE	Triticum aestivum		
ORGANISM	Triticum aestivum		
REFERENCE	Wang, H. X., Salmeron, J. M., Willits, M. G. and Lawton, K. A.		
AUTHORS	Monocotyledonous plant genes and uses thereof		
TITLE	Patent: WO 0166755-A 1 13-SEP-2001;		
JOURNAL	Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
source	1..4270		
exon	/organism="Triticum aestivum"		
intron	/db_xref="taxon:4565"		
exon	1396..2163		
intron	2164..2337		
exon	2338..2532		
intron	2533..2933		
exon	2934..3188		
BASE COUNT	1132 a	872 c	911 g 1355 t
ORIGIN			
Query Match	18.0%	Score 391.8;	DB 6; Length 4270;
Best Local Similarity	69.9%;	Pred. NO. 4.8e-90;	
Matches 528;	Conservative 0;	Mismatches 227;	Indels 0; Gaps 0;
Qy	781	TTTCAGACACACCTACTGGATATCTTGACAAAACCTGCAGCACACATGTAATGATGGTTT	840
Db	1412	TGCAGCGGATCTCCCTTGATTTCCCTTGATAAAGTTGAAGTGAACCTTCGGTTGATCT	1471
Qy	841	TATCTGTTGCAACATTTCTGGTAAAGCATGCGAGAGATTGCTTTCAAGCTCATTTGAG	900
Db	1472	TATCTGTTGCAACATTTATGCAACAATCTTGGTGNAACCTGTTTCGAGAGATCGATGGAGA	1531

Qy	901	TTATTGCTCAAGTCTAATGTTGATATCATACCCCTTGATAAAGCCTTGCTCATGACATTG	960
Db	1532	TGCTAGTCCGGTCAAAATCTTGACATGATTACTCTAGAGAAAGCATTGCTCTCAAGATGCA	1591
Qy	961	TAAAACAAATTTACTGATTCACGAGCGGAACCTTGGTCTACAAAGGCTGAAACCAAGGTT	1020
Db	1592	TCAAGCAAAATTTACTGATTTACGGATTAACCTTTGGATTAGCTTCACCCGAAGACAATGGCT	1651
Qy	1021	TTCTGATTAACATGTTTAAAGGATACATAGGCACTTGGATCTTGATGATTTGTAATTAC	1080
Db	1652	TTCTTAACAACACGTAAGAGGATACTCAGAGCACTTCTGATTCATGATGTTGGAGCTTG	1711
Qy	1081	TACAAATGTTGCTAAGAGAGGGGCATACCTACCTAGATGATGATGATGATCTCCATTATG	1140
Db	1712	TCAGGATGCTGCTCACAGAGGGGCACTAAACCTTGTGATGATGATGATGATGATGATG	1771
Qy	1141	CTGTAGGCTATTCGGATGCAAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGATA	1200
Db	1772	CTGTAGAACACTGTGACTCAAAAATTTACAAGAACTTCTGGACATCGCACTTGGGATG	1831
Qy	1201	TTAATCATCAAAAATTTCAAGGGGATACACGCTGCTGCATGTTGCAGCCATGAGGAAGAGC	1260
Db	1832	TTAATCTCAGAAACCCCAAGAGGTTTACTGTTCTTCAACATCGCCGCTAAAGCGAGAGATC	1891
Qy	1261	CTAAATGTTAGTGTCCCTTTTAAACAAAGGAGCTAGACCTTCTGATCTGACATCCGATG	1320
Db	1892	CTAAATCGTGTGCTCCCTTTTAAACAAAGGTCGCCGCTTCAGATTTTACATTTGATG	1951
Qy	1321	GAAGAAAGCACTTCAAAATCGCAAGAGGCTCACTAGGCTTGTGGATTTTCAGTAAGCTTC	1380
Db	1952	GAAGAAAGCAGTTCAAAATCTCAAGAGACTCAAAACATCGTGATTTTGGGAATA	2011
Qy	1381	CGGAGGAAGGAAAATCTGCTTCGAATGATCGGTTATGCATTTGATGATTTGGAGCAAGCAG	1440
Db	2012	CTGAAGAAGCAAGCCGCTCCCAATGATAAATATGATGATGATGATTTGGAGCAAGCTG	2071
Qy	1441	AAAGAAGAGACCCCTGCTGCTAGGAGAGCTTCTCTATCTTCTGCTATGCGAGCGATGAT	1500
Db	2072	AAAGAAGGATCCACAACCTTGGAGAGCACTACTTCTCTGCTATGCTGCTGCTGCTGCTC	2131
Qy	1501	TGCTATGAAGCTGTTTATACCTTGAATAATAGAGTT	1535
Db	2132	TTGCTGAAGAGTTACTGTACTCTTGAACCGAGGT	2166
RESULT 11			
AP002537/c			
LOCUS	AP002537	140304 bp	DNA linear PLN 26-JAN-2001
DEFINITION	Oryza sativa genomic DNA, chromosome 1, PAC clone: P0001B06.		
ACCESSION	AP002537		
VERSION	AP002537.2	GI:10934069	
KEYWORDS	Oryza sativa (cultivar: Nipponbare) DNA, clone: P0001B06.		
SOURCE	Oryza sativa		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
TITLE	Ehrhartoideae; Oryzeae; Oryza.		
JOURNAL	1 (bases 1 to 140304)		
REFERENCE	Sasaki, T., Matsumoto, T. and Yamamoto, K.		
AUTHORS	Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC		
TITLE	clone: P0001B06		
JOURNAL	Published Only in DataBase (2000) In press		
REFERENCE	2 (bases 1 to 140304)		
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-JUN-2000) Takuji Sasaki, National Institute of		
REFERENCE	Agrobiological Resources, Rice Genome Research Program; Kannondai		
AUTHORS	2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
TITLE	(E-mail: tsasaki@agr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,		
JOURNAL	Tel: 81-298-38-7441, Fax: 81-298-38-7468)		
COMMENT	On Oct 19, 2000 this sequence version replaced gi:8698575.		
	Genes were predicted from the integrated results of the following:		
	GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor		

(October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTp2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0001B06 clone has an overlap with P0671B11 (DBJ:AP002746) clone at the position 1 to 61357 of 5' end. The sequence of this clone starts at the position 107016 of P0671B11. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html> Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

FEATURES

source

```
1. .140304
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
/clone="P0001B06"
join(2486..2566,4546..4833)
/gene="P0001B06.1"
join(2486..2566,4546..4833)
/gene="P0001B06.1"
/note="hypothetical protein"
/codon_start=1
/protein_id="BAB16848.1"
/db_xref="GI:10934070"
/translation="MARENLTLSRDTPARQDTDRIGLGKEYSAHWQFALCLANLD
GLHRCALGAHNSLCRVLHHEVWESEAAAAAEEAEDRALRGIAVGLLGR
WQPOQECRSKRLTISCTPLH"
7047..7694
/gene="P0001B06.2"
7047..7694
/gene="P0001B06.2"
/note="hypothetical protein"
/codon_start=1
/protein_id="BAB16849.1"
/db_xref="GI:10934071"
/translation="MEVAGRTVAAAGGGGIGGARTAEAGLACPRCESTNTRFCY
YNNYLAQPRHFCACRRYVTRGGLRNVPGGTRNKVAPACPTGRKRRAAHHAA
APPTTTASSAPLPLMPAVAYELPPLPPPLPLAAVDPDRLLDLGGSTSLAPA
QLHNGHFTGFLGTWSSAPPPPPATSTPSPAHPVSDSIWAGWPHLSI"
join(8873..9730,9790..10095)
/gene="P0001B06.3"
join(8873..9730,9790..10095)
/gene="P0001B06.3"
/note="hypothetical protein"
/codon_start=1
/protein_id="BAB16850.1"
/db_xref="GI:10934072"
/translation="MEPQGPSETALPAPMVLPPPPPSDEAAAAEEBAGVKPDRQS
SSSSSSSEEEKSKDVAVETSVVPSVAASPDDEAAVAASGGDVIKHDEAV
VRPDWASWPQACTVDVAAAATTPQAPEIQTMSIQAPAAVAGFDPETPKSIFO
AKPGSSSOAEWSVNESLSFSIHHCARESGDLCGYAGESRSHFDYFDENAGGAAG
DHTSDWKLTVAEGSPGSARDATDGGGAQKQAKIDFRHESGSGAGSSGFSFAF
PYADDAIVIGDDDVAAEEGLRDVPSAEEGGGAAGVAGVGRDGDAGGAAAA
AELVLLRLVLLRVLLVYVLLVLLFVAVYQLQLQLNLLPLQLVPLCS"
complement(join(10657..11559,12026..12523))
/gene="P0001B06.4"
complement(join(10657..11559,12026..12523))
/gene="P0001B06.4"
/note="hypothetical protein"
```

gene

CDS

gene

CDS

gene

CDS

```
/codon_start=1
/protein_id="BAB16851.1"
/db_xref="GI:10934073"
/translation="NSADGGDFDLSIPAAIADVLGRVADGADIYAAXCLASRAFLAAS
YACSVHLRAALARRRSVALAGGGGGPGGSAIRAAAGNAASLIGPHLKSLELDAS
EOWGHPDQATVVEGEFDEGGDLHTAREAVVADTAAGNALREVADVWPOSCNR
KAEALPSIWSLTLVWSQIETSAIHAGLSLLKRLKNALWSVDGLKTMPLNTHLTFEIR
LDEDELKLNIECFPCQLIINLTIGVGLKDPKTHLQKLTCHWEVNSVRSITIRAPNL
VRLLEKCVRPDMLILDTPSMFTLKTVDKLGPNQVADGLVSLKLNRIEISLDLSILOV
PAENHDITTELELPTSTNKYELFAVKPEYLQIFAGISEVKLAPRSCENTHCLML
CTSNQFRCLRRLLFHLPLKDPVHLAPLNNCAPSCEVTILFHADSDDDIRQAATSV
WTLRPGIRWQGTWN"
complement(join(14597..14704,14802..14932,15057..15223,
15388..15503,15664..15819,16008..16116,16591..16700,
17245..17430,17515..18105))
/gene="P0001B06.5"
complement(join(14597..14704,14802..14932,15057..15223,
15388..15503,15664..15819,16008..16116,16591..16700,
17245..17430,17515..18105))
/gene="P0001B06.5"
/codon_start=1
/product="putative RNA methyltransferase"
/protein_id="BAB16852.1"
/db_xref="GI:10934074"
/translation="NATAAAAAAFAFPLRRRLPLHHRGRLLAAVAALSPEPPAPTP
TTSPPPPKGYFPRKNEVLETCGLAFKGCVRVDGSTFVLICDGLPGERLLAR
VRIIRGAFAPAAKLRTEPHRDADVAPCLAADCGCAQSLAAQIRHKHLQVRE
LLVNFPGKDPKRMESSEPDAILKPIVPCDEIFRYRNKMEFSFGTKRMQREWKKEKD
EVVKEEVEGDSYSLGHAPGDFDKLVHVEKLLQSEPADKVAIVQETWLDPAIGLT
PYDVHKHVGFLKHLMIRTGRNITTGAPVWVNFVTSYCPLELLEVNITIKIPVVS
IMNVNTSVGTEVEEYTLGKPTITEMRLGLTFQISANSFFTQTKQADLYKLII
GESAGLKDGSEIILDLCGTGTGLTLARRAKHVYGVYVPEAIAADAKKNKINGLS
NATVQGLNLKINETFGFKPKPDIIISDPNRPGMHMKLIKWLELVKAPRIVYVSCNP
ATCARDLYLCHGVEEKLKGVELKTVIPVDMPEPTTHIEICIVLELC"
join(19026..19092,19440..19762)
/gene="P0001B06.6"
join(19026..19092,19440..19762)
/gene="P0001B06.6"
/note="hypothetical protein"
/codon_start=1
/protein_id="BAB16853.1"
/db_xref="GI:10934075"
/translation="MHASDDNRTEGVAEAEEREREVAHRRHRRVGVSTPEAMSLIGFDI
VEKGGDDSGRSTCPAAAYVSRGLENTVLAAYQIQLSGEMLRRRRRPGDWPLL
LSRGPPHVAPLPQVTVRRYFSRRPPA"
join(22508..22615,22741..22836,22932..22994,23274..23351,
23884..24052,24235..24618,25397..25480,25581..25726,
26248..26508,26585..26766,26859..27141,28140..28334,
28526..28741,28826..28978,29068..29265)
/gene="P0001B06.7"
join(22508..22615,22741..22836,22932..22994,23274..23351,
23884..24052,24235..24618,25397..25480,25581..25726,
26248..26508,26585..26766,26859..27141,28140..28334,
28526..28741,28826..28978,29068..29265)
/gene="P0001B06.7"
/note="hypothetical protein"
similar to Arabidopsis thaliana chromosome 3, F22P7.18"
/codon_start=1
/protein_id="BAB16854.1"
/db_xref="GI:10934076"
/translation="MGPAKGSRTITKITIGYDDRDHEDPNSSSKVLKKRMSDLG
POWSKDELMREYAYRRHKNWKKVYASGKGSADTVEALYVSHRTLELSPERGATM
GFVALVTGHHNVDSKSHGSDQTVASGKVRKREATGQKEKPAHRSHERHTS
GLSFKRYGELYKNTPRHPSGKTRTPVPVFPADMNVAHAGINCTKKAAS
GATNLEKCSHGSGISESAKFVQGTFLFAKGTSLKKRRIQSMEOQOTIKDEHK
TAMVAKCNDTEYORLNTLPSDEMLVDLVLESLVTPVPSKISPKINIPSGTLGRDD
SALSHRREGSPVSRKQGVGSCASKTRNKRKLLIAEIVTEGVTSNHLLDPEE
RQVATSCALNSDLERGTVDLPSTANISTIKIPDLQSLKPEINMSRRSKSKSPCG
SKYVYNGADNLQARLQHCLSSLSLRWCYTFEYFSAVDIPWFMDFEYNYLFANL
SHLSRLTRSEWSTIRSLGKPRFSDHFLAAEKEDJENYKRYQYFALISESDSL
PPDLARPFISGGQVIVRSTRELCDGVMEQDRYNVQFDRPDGLVDGVKOTDCMP
VNWLDNLPDDLKRSFLSNNSHNRVEEQIPKFTSKENWDHISGEALSPSKMTHTSDE
```


Query Match		17.3%	Score 376.4;	DB 8;	Length 168372;
Best Local Similarity		66.3%;	Pred. No. 4.5e-86;		
Matches 542; Conservative		0;	Mismatches 276;	Indels	0; Gaps 0;
QY	781	TTCCAGAGACACCTACTGGATATCTTGACAAACTCGCAGCAGACGATGTAATGATGGTTT	840		
Db	162296	TGCAGGGCGGTCTCTTGATGTCCTTGATAAGTTGAGGTAGATTAACCTTCTATTGATCT	162237		
QY	841	TATCTGTTGCCAAACATTTGTGTAAGCATCGCAGAGATTGCTTTCAAGCTGCATTGAGA	900		
Db	162236	TATCTGTTGCCAACTTATGCAACAAATCTTGCAAGAACTGCTTGAAGATGCTTTGATA	162177		
QY	901	TTATTGTCAAGTCTAATGTTGATATCATACCCCTTGATAAAGCCTTGCCCTCATGCAATG	960		
Db	162176	TGGTAGTCCGGTCAAACTTGACATGATTACTCTTGAGAAAGTCATTGGCCTCCAGATGTTA	162117		
QY	961	TAAACAAATTAATGATTCACGAGCGGNACTTGTCTTACAAGGCCCTGAAAGCAACGGTT	1020		
Db	162116	TCAAGCAGATTAATGATGCACGCCCTAAGCCTTCGGATTAATTTCAACAGAAACAAGGAT	162057		
QY	1021	TTCTTGATAAATGTTAAGAGGATACATAGGCAATTTGGATTCTGATGATGTTGAATTAC	1080		
Db	162056	TTCTTAACAAACATGTGAGGAGGATACACAGAGCCCTTGACTCTGACGATGTAGACTAG	161997		
QY	1081	TACAAATGTTCTAAGAGAGGGGCATACCTACCTAGATGATGATATGCTCTCCATTATG	1140		
Db	161996	TCAGGATGCTGCTCACTGAAGGACAGACAATCTTGATGATGCGTTTGGACTGCACTAGC	161937		
QY	1141	CTGTAGCGTATGGCATGCAAGAGACTACACAGAACTTCTAGATCTTGCACTTGTCTGATA	1200		
Db	161936	CCGTGCAACATTTGACTTCCAAAATTACAACCGAGCTTTTGGATCTCGCACTTGCAGATG	161877		
QY	1201	TTAATCATCAAAATTCAGGGGATACAGGTCGTGCACTGTTGCGAGCATGAGAAAGAC	1260		
Db	161876	TTAATCATAGAAACCAAGAGGTTATCTGTTCTTCACTTGTGCGAGGCGAAGAGAC	161817		
QY	1261	CTAAAATTTGATGTCCTTTTAAACCAAGAGCTAGACCTTCTGATCTGACATCCGATG	1320		
Db	161816	CTAAAATCATTTCTCCTTTTAAACCAAGGGGCTCGGCCAGCAGATGTTACATTCGATG	161757		
QY	1321	GAAGAAAGCACTTCAAAATCGCAAGAGGCTCACTAGGCTTGTGGATTTTCAGTAACTCTC	1380		
Db	161756	GGAGAAAGCGGTTCAATCTCAAAAGACTTAACAAACAAAGGGGATTTACTTTGGGGTTA	161697		
QY	1381	CGGAGGAAGGAAATTCCTGCTTCGAATGATCGGTTTATGCAATGATGTTGGAGCAAGCAG	1440		
Db	161696	CGAAGAAGGAAACCTTCTCCAAAAGATAGGTTATGTTATTTGAATACTGGAGCAAGCTG	161637		
QY	1441	AAAGAGAGACCTCTGCTAGGAGAGCTTCTGATCTCTTGTCTATGGCAGGCGATGATT	1500		
Db	161636	AAAGAAGGAGCCCAACTCGGAGAAGCATCAGTTTCTTGTGAATGGCAGGTGAGAGTC	161577		
QY	1501	TGCGTATGAAGCTGTTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTTCCAA	1560		
Db	161576	TACGAGGAAGGTTGCTGATCTTGAACCGAGGTAACCTTTCACATATATCATATGGGT	161517		
QY	1561	TGGAAGCTTAAAGTTGCAATGGACATTCGCTCAAGTTGAT	1598		
Db	161516	TCATAATGCTGGTTCTTTTGGAAATTAAGTTTGGT	161479		
RESULT 13					
LOCUS	AR087501				
DEFINITION	Sequence 1 from patent US 5986082.				
ACCESSION	AR087501				
VERSION	AR087501.1 GI:10014264				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 5655)				

AUTHORS		Uknes, S. Joseph, Hunt, M. Denise, Steiner, H. and Ryals, J. Andrew.	
TITLE		Altered forms of the NIM1 gene conferring disease resistance in plants	
JOURNAL		Patent: US 5986082-A 1 16-NOV-1999;	
FEATURES		Location/Qualifiers	
source		1..5655	
BASE COUNT		1758 a 1014 c 1069 g 1814 t	
ORIGIN			
Query Match		15.0%;	Score 326.8; DB 6; Length 5655;
Best Local Similarity		58.6%;	Pred. No. 2.7e-73;
Matches 714; Conservative		0;	Mismatches 392; Indels 112; Gaps 4;
Qy	415	CGGAGTTTGCATCTTCGCGGAGCTTAAGCTTGTGGTTTCCGGCCGCTGAAGGAAATTC	474
Db	2962	CGCCGGATGATTTCTACGAGCGCTTAAGCTTGTCTCTCCGAC---GGCCGGGAAGTTT	3018
Qy	475	CGGTGCACCGGTGCATTTTGTGCGGAGGAGTCCGTTCTTTAAGAATTTGTTCTCGGTA	534
Db	3019	CTTTCCACCGGTGCGTTTGTCAAGGAGAGCTCTTCTTCAAGAGCGCTTTAGCGCGG	3078
Qy	535	AAAGAGAGAAATAGTAGT-----AAGTGGAAATGAAGGAGGTGA	576
Db	3079	CTAAGAAGGAGAGAAAGACTCCAACACACCGCGCGTGAAGCTCGAGCTTAAGGAGATTG	3138
Qy	577	TGAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTGTATAGTG	636
Db	3139	CAAGGATTACGAAGTCGGTTTCGATTCGGTTGACTGTTTGGCTTAGTTTACAGCA	3198
Qy	637	GTAAGTTTAGGCTTCACCTAAAGATGTGTGTTTGTGTGGACAATGACTCTCTCATG	696
Db	3199	GCAGAGTGAGACGCGCGCTTAAAGGAGTTTCTGAATGCGACAGAGAAATTCGCCAG	3258
Qy	697	TGCTTGTAGGCGAGCTGTGGCATTCCTCGTTGAGGTTTGTACACATCATTTACTTTC	756
Db	3259	TGGCTTGGCGCGCGGTGGATTTTCATGTTGAGGTTCTCTATTGGCTTTCATCTTCA	3318
Qy	757	AGATCTCTGAAT-----	768
Db	3319	AGATCCCTGAATTAATTAATCTCTATCATCAGTAACACCATCTGCATTAAGCTATGGTTA	3378
Qy	769	-----TGGTTGACAAGTTTCAGAGACACCTACTG	797
Db	3379	CACATTTCATGAATATGTTCTTACTTTCAGTACTGTTGTTTGTATTTCAGAGGCATTAATG	3438
Qy	798	GATATTCTTGACAAAACCTCCAGCAGCATGTAATGATGGTTTATCTGTTGCAACATT	857
Db	3439	GACGTTGTAGACAAAGTGTATAGAGACACATTTGGTTTATCTCAAGCTTCTTAATA	3498
Qy	858	TGTGTAAAAGCATCGAGAGATTTGCTTTCAAGCTGCATTGAGATTATTGTCAGTCTAAT	917
Db	3499	TGTGGTAAAGCTTGTAAGCTATTGGATAGATGTAAGAGATTATTGTCAGTCTAAT	3558
Qy	918	GTTGATATCATAAACCTTGATAAAGCCTTGCCTCATGACATTTGTAACAAATTAATGAT	977
Db	3559	GTAGATATGTTAGTCTTGAAGAAGTCATTTCGCGAAGAGCTTGTGTTAAAGAGATAATGAT	3618
Qy	978	TCAGAGCGGAACCTTGGCTCTACAAGGCCCTGAAACGAGCGTTTCCCTGATAAAGCATGTT	1037
Db	3619	AGACGTAAGAGCTTGGTTTGGAGGTACCTAAAGTAAG-----AAACATGTC	3666
Qy	1038	AAGAGATACATAGGCGATTGGATTCTGATGATGTTGAATTAATTAATTAATTAATTAATTA	1097
Db	3667	TCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTAGCAAGTTGCTTTTGA	3726
Qy	1098	GAGGCGCATACTACCCCTAGATGATGATGCTCTCCATTATGCTGAGCGTATTGCGAT	1157
Db	3727	GAGGATCACACCAATCTAGATGATGCTGCTCTTCATTTGCTGTTGATATTGCAAT	3786
Qy	1158	GCAAGAGCTACAGCAAGCTTCTAGATCTGACCTTGTGCTTGTGCTTGTGCTTGTGCTTGT	1217
Db	3787	GTGAAGCGCCACACAGATCTTTTAAACCTTGATCTTGGCGATGTCACCATAGGATCCG	3846

```
QY 1218 AGGGATACACGGCTGCATGTTGTCAGCCATGAGGAAGAGCCTAAATTTAGTGTCC 1277
|||||
Db 3847 AGGGATATACGGTGCTTCATGTTGCTGCGATCGGAAGGAGCACAATTCATCATATC 3906
QY 1278 CTTTAAACAAAGGAGCTAGACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAA 1337
|||
Db 3907 CTTATGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGTGAAGCCGCACTCATG 3966
QY 1338 ATCGCCAAAGAGGCTCAGTACGCTTGTGGATTTCAAGTTCAGTTCGGAAGGAGGAAAAATCT 1397
|||||
Db 3967 ATCGCAAAACAAAGCCACTATGCGCGTTGAATGTAATATATCCCGAGCAATGCAAGCAT 4026
QY 1398 GCTTCGAATGATCGGTATGCATTCATGAGATCTGAGCAAGCAGCAAGAAAGACCCCTCTG 1457
|||
Db 4027 TCTCTCAAGGCCACTATGTTGTAATACTAGAGCAAGAAAGCAACGAGACAAAT 4086
QY 1458 CTAGAGAGAGCTTCTGATCTCTTCGATGCGCAGCGGATGATTTCGCTGAAGCTGTGA 1517
|||
Db 4087 CCTAGAGATGTTCTCTCTCTTTGCAAGTGGCGCGCATGAATTTGAAGATGACGCTGCTC 4146
QY 1518 TACCTTGAATAAGATT 1535
|||||
Db 4147 GATCTTGAATAAGAGT 4164

RESULT 14
LOCUS ATU87794
DEFINITION Arabidopsis thaliana transcription factor inhibitor I kappa B
U87794
ACCESSION U87794
VERSION 1
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,
Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and
Uknes,S.
The Arabidopsis NIM1 protein shows homology to the mammalian
transcription factor inhibitor I kappa B
JOURNAL Plant Cell 9 (3), 425-439 (1997)
MEDLINE 97246324
REFERENCE 2 (bases 1 to 5655)
AUTHORS Ryals,J., Weymann,K., Lawton,K., Friedrich,L., Ellis,D.,
Steiner,H.-Y., Johnson,J., Delaney,T.P., Jesse,T., Vos,P. and
Uknes,S.
Direct Submission
JOURNAL Submitted (29-JAN-1997) Fungicides, Novartis BGC, 3054 Cornwallis
Road, Research Triangle Park, NC 27709, USA
FEATURES
source
1. .5655
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
/map="between ATHGENEA and ngall1"
join(2754. .3347,3427. .4162,4271. .4474,4586. .5053)
2787. .4866
/gene="nim1"
join(2787. .3347,3427. .4162,4271. .4474,4586. .4866)
/gene="nim1"
/codon_start=1
/product="transcription factor inhibitor I kappa B
homolog"
/protein_id="AB58262.1"
/db_xref="GI:1916912"
/translation="MDTIDGPDVSVFATDNTDSSIVYLAAAEQVLTGPDVS
ALQLLSNSPESVFDSPDDFYSDAKLVLSDGREVSFHRVLSARSSFFKSALAAAKKEK
```

```
BASE COUNT 1758 a 1014 c 1069 g 1814 t
ORIGIN
Query Match 15.0%; Score 326.8; DB 8; Length 5655;
Best Local Similarity 58.6%; Pred. No. 2.7e-73;
Matches 714; Conservative 0; Mismatches 392; Indels 112; Gaps 4;
QY 415 CGAGGTTTACATTCGCGCGAGCTTAAGCTTGTGGTTTCCGCCGCGTGAAGAAATTC 474
|||
Db 2962 CGCCGATGATTTCTACAGGAGCTTAAGCTTGTCTCTCCGAC--GGCCGGAGATT 3018
QY 475 CGGTGCACCGGTGCATTTTGTGCGGAGGAGTCCGTTCTTTAAGAAATTTGTCTCGGTA 534
|||
Db 3019 CTTTCCACCGGTGCGTTTGTGTCAGGAGAGCTCTTTCTCAAGAGCGCTTTAGCCGCG 3078
QY 535 AAAAGGAGGAATAGTACT-----AAGGTGGAATTTGAAGGAGTGA 576
|||
Db 3079 CTAAGAAGGAGAAAGACTCCAACAACACCGCGCGTGAAGCTCGAGCTTAAGGAGATTG 3138
QY 577 TGAAGAGCATGAGGTGAGCTATGATCTGTAATAGTGTATTGGCTATTGTGTATAGTG 636
|||
Db 3139 CCAAGGATTACGAAGTCGGTTTCGATTCGGTTGTGACGTGTGTGCTATGTTACAGA 3198
QY 637 GTAAAGTTAGGCTTACCTAAAGATGTGTGTGTGTGGACAATGACTCTCTCATG 696
|||
Db 3199 GCAGAGTGAGACGCGCGCTAAAGGAGTTCTGTAATGCCAGACAGAAATTCCTCCACG 3258
QY 697 TGGCTTGTAGGACGCTGCGCATTCCTGGTTGAGGTTTGTACACATCAITTACTTTC 756
|||||
Db 3259 TGGCTTGGCGCGCGGCGGTGGATTTCAATGTGGAGGTTCTCTATTGGCTTTTCATCTCA 3318
QY 757 AGATCTCTCGAAT-----AAGGTGGAATTTGAAGGAGTGA 768
|||||
Db 3319 AGATCCCTGAATTAATTACTCTATCAGGTAACAACCACTGCAATTAAGCTATGGTTA 3378
QY 769 -----TGGTGACAAAGTTTCAGAGACACCTACTG 797
|||
Db 3379 CACATTCATGAATATGTTCTTACTTCAAGTCTGATTTATGTTTCAAGGCACTATTG 3438
QY 798 GATATTCTTGACAAACTGCACGACGATGTAATGATGTTTATCTGTTGCAACAAT 857
|||
Db 3439 GAGTTGTAGACAAAGTTGTTATAGGAGACACATTTGGTTATCTCAAGCTTGCTAATA 3498
QY 858 TGTGTAAGCATGGGAGAGATTGCTTCAAGCTCATTTGAGATTATTGTTCAAGTCTAAT 917
|||||
Db 3499 TGTGTAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATATTGTCAAGTCTAAT 3558
QY 918 GTTGATATCATAAACCTTGATAAAGCCTTGCCCTCATGACATTTGTAACAAATTTACTGAT 977
|||
Db 3559 GTAGATATGGTTAGTCTTGAAAGTCATTTGCCGGAAGAGCTGTTTAAAGAGATAATTGAT 3618
QY 978 TCACGAGCGGAACCTTGGTCTACAAAGGCGCTGAAAGCAACGGTTTTCCTGATAACATGTT 1037
|||
Db 3619 AGACGTAAGAGCTTGGTTTGGAGGTACCTAAAGTAAG-----AAACATGTC 3666
QY 1038 AAGAGGATACATAGGCGCATTTGGATTCTGATGTTTGAATTACTACAATTTGTTGTAAGA 1097
|||
Db 3667 TCGAATGTACATAAGGCACCTTGACTCGGATGATATTGAGTTAGTCAAGTTCCTTTGAAA 3726
QY 1098 GAGGGCATACTACCCCTAGATGATCATATGCTCTCCATTATGCTGTAGCGTATTGCGAT 1157
|||
Db 3727 GAGGATCACACCACTAGATGATGCGTGTCTCTTCATTTTCGCTGTTGTCATATTGCAAT 3786
QY 1158 GCAAGACTACAGCAGCACTTCTAGATCTTGCATTTGCTGATATTATCATCAAAATCA 1217
```


D _b	89267	I GTGAAGACCGCAACAGATCTTTAAAACTTGACTCCGATGTCAACCATTAGAATTCG	89326
Q _y	1218	AGGGGATACACGGTGCCTCATGTTTGCAGCCATTGAGAAAGAGCCTAAAATTGTAGTGTCC	1277
D _b	89327	AGGGGATATACGGTGCCTTCATGTTGCTCGCATCGGAAGAGGCCACAATTGATACTATCT	89386
Q _y	1278	CTTTTAACCAAAGAGCTAGACCTTCGTGATCTGCATCCGATGGAAGAAAAGCACTTCAA	1337
D _b	89387	CTATTGGAAAAGGTGCAAGTGCATCAGAACAACCTTTTGGAAAGGTAGAACCGCACATG	89446
Q _y	1338	ATCGCCAAGAGGCTCACTTAGGCTTGTGGATTCTAAGTAAGTCTCCGGAGGAAGAAAATCT	1397
D _b	89447	ATCGCAAAACAAGCCACTATGCGCGTTGAATGTATAATATCCCGGAGCAATGCAAGCAT	89506
Q _y	1398	GCTTCGAATGATCGGTTATATGCATTGAGATTCTTGAGCAGCAGCAANAAGAGACCCCTCTG	1457
D _b	89507	TCTCTCAAGGCCGACTATGTGTAGAATACTAGAGCAAGAAGACAACGAGACAACAAAT	89566
Q _y	1458	CTAGGAGAAGCTTCTGTATCTTCTTGTATGGCAGGCATGATTTTTCGATATGAAGCTTTA	1517
D _b	89567	CCTAGAGATGTTCTCCCTCTTTTTGCAGTGGCGCCCATGAATTGAAGATGACCTGCTC	89626
Q _y	1518	TACCTTGAATAATAGATT	1535
D _b	89627	CATCTTGAATAATAGAGT	89644

Search completed: October 8, 2002, 00:43:29
Job time : 3175.43 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 21:14:44 ; Search time 235.181 Seconds
(without alignments)
15856.428 Million cell updates/sec

Title: US-08-908-884-13
Perfect score: 2172
Sequence: 1 GTGACTTCTACTATGGCT.....ATTGAAAAAAAAAAAAA 2172

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES			Description
	Score	Match	Length DB	
1	2172	100.0	2172	19 AAV16852 Nicotiana glutinosa
2	1767	81.4	1767	21 AAA97190 N. tabacum NIM1 ho
3	1380.4	63.6	1731	21 AAA97191 L. esculentum NIM1
4	781.2	36.0	2299	21 AAA97229 B. vulgaris NIM1 h
5	620.6	28.6	659	21 AAA97211 N. tabacum NIM1 ho
6	581.6	26.8	2024	21 AAC37765 Arabidopsis thalia
7	578.4	26.6	2104	19 AAC16851 Arabidopsis thalia
8	576.8	26.6	2011	19 AAV46274 A. thaliana NIM-1
9	576.8	26.6	2011	19 AAV46275 A. thaliana NIM-1

10	576.8	26.6	2011	19	AAV43661	Non-inducible immu
11	575.4	26.5	653	21	AAA97219	S. tuberosum NIM1
12	563.4	25.9	2040	22	AAC81457	Rice NPR1 homologu
13	558.6	25.7	2194	21	AAA61047	Rice putative nega
14	549.4	25.3	1597	19	AAV46276	A. thaliana N-term
15	549.4	25.3	1597	19	AAV43662	Non-inducible immu
16	527.6	24.3	1668	22	AAH43384	cDNA sequence enco
17	517.4	23.8	1608	19	AAV46277	A. thaliana C-term
18	517.4	23.8	1608	19	AAV43663	Non-inducible immu
19	513.8	23.7	1803	21	AAA97202	A. thaliana NIM1 h
20	513.8	23.7	1818	21	AAA97233	A. thaliana NIM1 h
21	513	23.6	1565	22	AAH43382	cDNA sequence enco
22	490	22.6	1194	19	AAV46278	A. thaliana C- and
23	490	22.6	1194	19	AAV43664	Non-inducible immu
24	467.2	21.5	1740	21	AAA97192	B. napus NIM1 homo
25	432.4	19.9	498	21	AAA97215	L. esculentum NIM1
26	391.8	18.0	4270	22	AAH43377	DNA sequence enco
27	362.4	16.7	2673	21	AAA97234	N. tabacum NIM1 ho
28	330	15.2	498	21	AAA97216	B. vulgaris NIM1 h
29	328.8	15.1	2844	21	AAA97230	H. annuus NIM1 homo
30	326.8	15.0	5655	19	AAV46273	A. thaliana NIM-1
31	326.8	15.0	5655	19	AAV43659	A. thaliana non-in
32	326.8	15.0	5655	19	AAV04632	Arabidopsis thalia
33	326.8	15.0	7548	19	AAV16850	Arabidopsis thalia
34	326.8	15.0	9919	19	AAV43658	A. thaliana non-in
35	326.8	15.0	9919	19	AAV04631	Arabidopsis thalia
36	317	14.6	1428	22	AAC84339	Rice Nph1 protein
37	317	14.6	2368	22	AAC84340	Rice Nph1 cDNA seq
38	316.2	14.6	786	19	AAV46279	A. thaliana NIM-1
39	316.2	14.6	786	19	AAV43665	Non-inducible immu
40	315.4	14.5	2069	21	AAA61048	Rice putative nega
41	315.4	14.5	2326	22	AAH43381	cDNA sequence enco
42	302.4	13.9	1761	21	AAA97193	A. thaliana NIM1 h
43	300.8	13.8	2171	21	AAC46995	Arabidopsis thalia
44	290.4	13.4	1725	21	AAA97232	A. thaliana NIM1 h
45	288	13.3	498	21	AAA97217	H. annuus NIM1 homo

ALIGNMENTS

RESULT 1

AAV16852 standard; cDNA; 2172 BP.

AAV16852; AC

17-AUG-1998 (first entry)

Nicotiana glutinosa NPR1 homologue.

NPR1 gene; acquired resistance; disease; plant pathogens; bacteria; mycoplasma; fungi; insects; nematodes; viruses; viroids; transgenic; homologue; ds.

Nicotiana glutinosa.

Key Location/Qualifiers

CDS 240..2006

FT /*tag= a

FT /product= acquired resistance polypeptide

FT /note= NPR1 homologue

XX WO9806748-A1.

XX 19-FEB-1998.

XX 08-AUG-1997; 97WO-US13994.

XX 16-MAY-1997; 97US-0046769.

XX 09-AUG-1996; 96US-0023851.

XX 10-JAN-1997; 97US-0035166.

Db 1741 TTGGAAACGCTTCTTTCCACGTTGTTTCAGAAAGTTCTAATAAGATCATGGATGCTGATG 1800
QY 1801 ACTTGCTCAGATAGCTTACATGGGAATGATACGGCAGAAGAGCGTCAACTGAAGAAGC 1860
Db 1801 ACTTGCTCAGATAGCTTACATGGGAATGATACGGCAGAAGAGCGTCAACTGAAGAAGC 1860
QY 1861 AAAGGTACATGGAACTTCAAGAAATCTCAGTAAAGCATTCACCTGAGGATAAAGAGAT 1920
Db 1861 AAAGGTACATGGAACTTCAAGAAATCTCAGTAAAGCATTCACCTGAGGATAAAGAGAT 1920
QY 1921 ATGATAAGACTAACACATCTCCTCATCTTGTCTCTACATCTAAGGAGTAGATAAGC 1980
Db 1921 ATGATAAGACTAACACATCTCCTCATCTTGTCTCTACATCTAAGGAGTAGATAAGC 1980
QY 1981 CCAATAGCTCCCTTTTAGAAATAGGTAAATGTTATAGGATATATAGGAAGAAGAGA 2040
Db 1981 CCAATAGCTCCCTTTTAGAAATAGGTAAATGTTATAGGATATATAGGAAGAAGAGA 2040
QY 2041 TTTTCTGTAACATAGCACTCTTCTTTCATCATTTGATATGTCAACATACATACAACA 2100
Db 2041 TTTTCTGTAACATAGCACTCTTCTTTCATCATTTGATATGTCAACATACATACAACA 2100
QY 2101 GCTGTACCATAACTGTTGTCACCTTACAACTTTGAAGAACAAGATTTATTGAAA 2160
Db 2101 GCTGTACCATAACTGTTGTCACCTTACAACTTTGAAGAACAAGATTTATTGAAA 2160
QY 2161 AAAAAAAAAA 2172
Db 2161 AAAAAAAAAA 2172

RESULT 2

AAA97190

ID AAA97190 standard; cDNA; 1767 BP.

XX AAA97190;

XX 25-JAN-2001 (first entry)

DE N. tabacum NIM1 homologue coding sequence SEQ ID NO: 1.

KW Systemic acquired resistance; SAR; signal transduction cascade;

KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;

XX potato; ss.

XX Nicotiana tabacum.

XX Key Location/Qualifiers

FH CDS 1..1767

FT /*tag= a

FT /product= "NIM1 homologue"

XX WO200053762-A2.

XX 14-SEP-2000.

XX 07-MAR-2000; 2000WO-EP01978.

XX 09-MAR-1999; 99US-0265149.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;

DR WPI; 2000-594322/56.

XX P-PSDB; AAB27301.

XX Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are

PT homologues of Arabidopsis NIM1 gene -

XX Claim 3; Page 68-70; 152pp; English.

Db 721 GTAAACAAATTTACTGATTCACGAGCGGAACCTTGGTCTACAAGGGCTGAAACACCGGT 780

XX

CC The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC gene and protein can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, perlaionium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize.

SQ Sequence 1767 BP; 512 A; 328 C; 434 G; 493 T; 0 other;

Query Match 81.4%; Score 1767; DB 21; Length 1767;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 ATGATAATAGTAGGACTGCGTTTCTGATTGGAATGACATCAGCGGAAGCAGTAGTATA 299

Db 1 ATGATAATAGTAGGACTGCGTTTCTGATTGGAATGACATCAGCGGAAGCAGTAGTATA 60

QY 300 TGCTGCATCGCGCGGCATGACTGAATTTTCTCGCGGAGACTTCGCGGGGAGATC 359

Db 61 TGCTGCATCGCGCGGCATGACTGAATTTTCTCGCGGAGACTTCGCGGGGAGATC 120

QY 360 ACTTCACTGAAACGCTATCGGAACACTGGAATCTTCTCGCGGAGACTTCGCGGGGAG 419

Db 121 ACTTCACTGAAACGCTATCGGAACACTGGAATCTTCTCGCGGAGACTTCGCGGGGAG 180

QY 420 TTTGACTACTTCGCGGACGCTAAGCTTGTGTTTTCGCGCCGCTGTAAGGAAATCCGGTG 479

Db 181 TTTGACTACTTCGCGGACGCTAAGCTTGTGTTTTCGCGCCGCTGTAAGGAAATCCGGTG 240

QY 480 CACCGGTGCATTTTGTGCGGAGAGTCCGTTCTTTAAGAAATTTGTTCTCGGTTAAAG 539

Db 241 CACCGGTGCATTTTGTGCGGAGAGTCCGTTCTTTAAGAAATTTGTTCTCGGTTAAAG 300

QY 540 GAGAAGAATAGTAGTAAGGTGGAATTTGAAGAGGTGATGAAGAGCATGAGGTGAGCTAT 599

Db 301 GAGAAGAATAGTAGTAAGGTGGAATTTGAAGAGGTGATGAAGAGCATGAGGTGAGCTAT 360

QY 600 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCCTTCACCTAAA 659

Db 361 GATGCTGTAATGAGTGTATTGGCTTATTTGTATAGTGGTAAAGTTAGGCCCTTCACCTAAA 420

QY 660 GATGCTGTTGTTGTGGACAATGACTGCTCATGTGGCTTTGAGGCCAGCTGTGGCA 719

Db 421 GATGCTGTTGTTGTGGACAATGACTGCTCATGTGGCTTTGAGGCCAGCTGTGGCA 480

QY 720 TTCCTGTTGAGGTTTTGTACACATCATTTACCTTTTCAGATCTCTGAATTTGTTGACAAG 779

Db 481 TTCCTGTTGAGGTTTTGTACACATCATTTACCTTTTCAGATCTCTGAATTTGTTGACAAG 540

QY 780 TTCAGAGACACCTACTGGATATTTTGACAAAATCTCAGCAGACGATGTAATGATGGTT 839

Db 541 TTCAGAGACACCTACTGGATATTTTGACAAAATCTCAGCAGACGATGTAATGATGGTT 600

QY 840 TTATCTGTTGCAACATTTTGTGTAAGCATGCGAGAGATTTGTTCAAGCTGCATTTGAG 899

Db 601 TTATCTGTTGCAACATTTTGTGTAAGCATGCGAGAGATTTGTTCAAGCTGCATTTGAG 660

QY 900 ATTATTGCTCAAGTCTAATGTTGATATCATAAACCTTTGATAAAGCCTTGCCCTCATGACATT 959

Db 661 ATTATTGCTCAAGTCTAATGTTGATATCATAAACCTTTGATAAAGCCTTGCCCTCATGACATT 720

QY 960 GTAAACAAATTTACTGATTCACGAGCGGAACCTTGGTCTACAAGGGCTGAAACACCGGT 1019

Db 721 GTAAACAAATTTACTGATTCACGAGCGGAACCTTGGTCTACAAGGGCTGAAACACCGGT 780

Qy	1020	TTTCTCTGATAAACATGTTTAAAGAGGATACATAGGGCATTTGGATTCTGATGATGTTGAATTA	1079
Db	781	TTTCTCTGATAAACATGTTTAAAGAGGATACATAGGGCATTTGGATTCTGATGATGTTGAATTA	840
Qy	1080	CTACAAATGTTGCTAAGACAGGGGCACTACTACCTTAGATGATGCATGCTCTCCCATTTAT	1139
Db	841	CTACAAATGTTGCTAAGACAGGGGCACTACTACCTTAGATGATGCATGCTCTCCCATTTAT	900
Qy	1140	GCTGTAGCGTATTTCGATCAAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGTAT	1199
Db	901	GCTGTAGCGTATTTCGATCAAAAGACTACAGCAGAACTTCTAGATCTTGCACTTGCTGTAT	960
Qy	1200	ATTAAATCATCAAAATTCAGAGGGATACAGGTGCTGCATGTTGCAGCCATGAGGAAGAG	1259
Db	961	ATTAAATCATCAAAATTCAGAGGGATACAGGTGCTGCATGTTGCAGCCATGAGGAAGAG	1020
Qy	1260	CCTAAAAATGTAGTGTCCCTTTTAAACAAAGAGAGCTAGACCTTCTGTATCTGACATCCGAT	1319
Db	1021	CCTAAAAATGTAGTGTCCCTTTTAAACAAAGAGAGCTAGACCTTCTGTATCTGACATCCGAT	1080
Qy	1320	GGAGAAAAGCACTTCAAAATCGCCAAAGAGGCTCACTAGGCTTGTGGATTTTCAGTAAGTCT	1379
Db	1081	GGAGAAAAGCACTTCAAAATCGCCAAAGAGGCTCACTAGGCTTGTGGATTTTCAGTAAGTCT	1140
Qy	1380	CCGAGGAGAGGAAATCTGCTTCGAATGATCGTTTATCATTGAGATTCGTGGAGCAAGCA	1439
Db	1141	CCGAGGAGAGGAAATCTGCTTCGAATGATCGTTTATCATTGAGATTCGTGGAGCAAGCA	1200
Qy	1440	GAAGAAGAGACCCCTGCTAGGAGAAGCTTCTGTATCTTGTCTATGGCAGCGCATGAT	1499
Db	1201	GAAGAAGAGACCCCTGCTAGGAGAAGCTTCTGTATCTTGTCTATGGCAGCGCATGAT	1260
Qy	1500	TTGCGTATGAAGCTGTTATACCTTGAAATAGAGTTGGCTGGCTTAACTCCCTTTTCCCA	1559
Db	1261	TTGCGTATGAAGCTGTTATACCTTGAAATAGAGTTGGCTGGCTTAACTCCCTTTTCCCA	1320
Qy	1560	ATGSAAGCTAAAGTTGCAATGGACATTCGCTAAAGTTGATGGCACTTCTGAGTTCCCACTG	1619
Db	1321	ATGSAAGCTAAAGTTGCAATGGACATTCGCTAAAGTTGATGGCACTTCTGAGTTCCCACTG	1380
Qy	1620	GCTAGCATCGGCAAAAAGATGGCTTAATGCACAGAGGACAAAGTAGATTTTGAACGAGGCT	1679
Db	1381	GCTAGCATCGGCAAAAAGATGGCTTAATGCACAGAGGACAAAGTAGATTTTGAACGAGGCT	1440
Qy	1680	CCTTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACCTCTCTAGAACTGTGAAA	1739
Db	1441	CCTTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACCTCTCTAGAACTGTGAAA	1500
Qy	1740	CTTTGGAAAAGCGTCTTTTCCAGCTGTTGCTCAGAACTTCTAAATAGATCATGGATGCTGAT	1799
Db	1501	CTTTGGAAAAGCGTCTTTTCCAGCTGTTGCTCAGAACTTCTAAATAGATCATGGATGCTGAT	1560
Qy	1800	GACTTGTCTCAGATAGCTTACATGGGGAATGATACGGCAGAGAGCGCTCAACTCAAGAAG	1859
Db	1561	GACTTGTCTCAGATAGCTTACATGGGGAATGATACGGCAGAGAGCGCTCAACTCAAGAAG	1620
Qy	1860	CAAAGGTACATGGAATCTCAAGAAATTCGACTTAAAGCATTTCACTGAGGATTAAGAAGAA	1919
Db	1621	CAAAGGTACATGGAATCTCAAGAAATTCGACTTAAAGCATTTCACTGAGGATTAAGAAGAA	1680
Qy	1920	TATGATAAGACTTAACAACATCTCCTCATCTTCTTCTTCTACATCTAAGGGAGTAGATAG	1979
Db	1681	TATGATAAGACTTAACAACATCTCCTCATCTTCTTCTTCTACATCTAAGGGAGTAGATAG	1740
Qy	1980	CCCAATAAGCTCCCTTTTATAGGAATAAG	2006
Db	1741	CCCAATAAGCTCCCTTTTATAGGAATAAG	1767

RESULT 3

AAA97191

ID AAA97191 standard; cDNA; 1731 BP.

```

XX AAA97191;
AC
XX
XX 25-JAN-2001 (first entry)
DT
XX
XX L. esculentum NIMI homologue coding sequence SEQ ID NO: 3.
DE
XX
XX Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW potato; ss.
KW
XX
XX Lycopersicon esculentum.
OS
XX
XX Key Location/Qualifiers
FH 1..1731
FT CDS /*tag= a
FT /product= "NIMI homologue"
FT
XX WO200053762-A2.
PN
XX
XX 14-SEP-2000.
PD
XX
XX 07-MAR-2000; 2000WO-EP01978.
PF
XX
XX 09-MAR-1999; 99US-0265149.
PR
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA
XX
XX Salmemon JM, Weislo LJ, Willits MG, Mengiste T;
PI
XX
XX WPI; 2000-594322/56.
DR
XX P-PSDB; AAB27302.
DR
XX
XX
XX
XX
XX Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIMI gene -
XX
XX Claim 3; Page 73-75; 152pp; English.
PS
XX
XX The present invention is concerned with the isolation of NIMI homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIMI is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC gene and protein can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidiodyne incognita. In particular they can be used against disease
CC organisms of maize.
XX
XX SQ Sequence 1731 BP; 508 A; 318 C; 408 G; 497 T; 0 other;

```

Qy	247	ATAGTAGGACTCGTGGTTCTTGATTCCGAATGACATCAGCGGAAGCAGTAGTATATGCTGCA	306
Dd	5	ATAGTAGAACTGCTTTTTTCGAATCCCAATCATATTAGTGGAACGAGTAGTATATGCTGCA	64
Qy	307	TGCGCGCGGCATGACGTGAATTTTTCTGCCGGGAGACTTCGCGCGGAGAGATCACTTCAC	366
Dd	65	TGAACGAAT-----CGGAAACTTCACCTGGCAGACGCTCAATTCCTC	103
Qy	367	TGAACCGCCTATCGGAACAACACTGGAACTCTATCTTCGATCGGCTCTTTGCCGGAGTTTGACT	426
Dd	104	TCAAACGCTCATCAGAACAACACTAGAGTCTATCTTCGATCGCTCTGGCGCGGATTTGCACT	163

Qy	427	ACTTCGCGGACGCTAAGCTTGTGGTTTTCGGGCCCGGTGAAGAAATTCGGTGCACCGGT	486
Db	164	TCTTCGTGATGCTAAGACTTCTGGCTCCACGC---GGTAAGGAAATTCGGTGCATCGGT	220
Qy	487	GCATTTTGTGCGGAGGAGTCCGTCCTTTAAGAAATTTGTTCTGCGGTAAAAAGGAGAAGA	546
Db	221	GCATTTTGTGCGGAGGAGTCCCTTTTAAAGAAATGTAATCTGTGGGAAA-----GATA	274
Qy	547	ATAGTAGTAAGGTGGAAATTAAGAGGAGTGTAAAGAGCATGAGGTGAGCTATGATGCTG	606
Db	275	GCAGCACGAAGCTGGAACATAAGAGCTGATCAAGAGATATGAGTGAATTTGATGCCG	334
Qy	607	TAATGAGTGTATTGGCTTAATTTGATAGTGGTAAAGTTAGGCTTCACCTAAAGATGTGT	666
Db	335	TGTCAGTGTGCTCGGCTATTTGTATAGTGGAAAAAGTTAGGCTGCATCTAAAGATGTGT	394
Qy	667	GTGTTGTGTGGCAATGACTGCTCATGTGCGCTTGTAGGCCAGCTGTGCAATTCCTGG	726
Db	395	GTGTTGTGTGGCAATGAGTGGTTCGATGTAGCTTGTAGGCCAGCTGTGCTTCATGG	454
Qy	727	TTGAGGTTTGTACACATCAATTTACCTTTTCAGATCTCTGAATTTGGTTGACAAGTTTCAGA	786
Db	455	TTGAGGTTTGTAGCATCCTTTACCTTTTCAGATCTCTCAATTTGTCGACAAGTTTCAGA	514
Qy	787	GACACCTACTTGGATATCTTTGACAAAGTGCAGCAGACGATGTAATGATGTTTATCTG	846
Db	515	GACACCTATTGGGATATCTTTGACAAAGCTGTAGCAGATGATGTAATGATGTTTATCCG	574
Qy	847	TTGCAACATTTCTGGTAAAGCATGCGAGCATTCCTTTCAAGCTGCATTCAGATTAATG	906
Db	575	TTGCAACATTTCCGGTAAAGCATGTGAAGATTTACTTTCAAGATGCAATGATATTAATG	634
Qy	907	TCAAGTCTAATTTGATATCATAACCTTTGATAAAGCCTTGCCCTCATGACATTTGATAAAC	966
Db	635	TCAAGTCTAATTTGATATCATAACCTTTGATAAAGTCTTGCCCTCATGACATTTGATAAAC	694
Qy	967	AAATTACTGATTCACAGCGGAACTTGTGCTACAAGGCGCTGAAGCAACGGTTTTCTG	1026
Db	695	AAATTACTGATTCACGCTGCTGAACCTTGTGCTCAAGGCGCTGAAGCAATGGTTTTCTG	754
Qy	1027	ATAAATGTTAAGAGCATACATAGGCAATTCGATTTCTGATGATGTAATTTACTACAAA	1086
Db	755	ATAAATGTTAAGAGCATACATAGGCAATTTGGACTCTGATGATTTGAATTTACTAAGGA	814
Qy	1087	TGTTGCTAAGAGGGGCATCTACCTAGATGATGCATATGCTCTCCATTTACTGCTAG	1146
Db	815	TGTTGCTTAAAGAGGGGCATCTACTCTTGATGATGCATATGCTCTCCATTTACTGCTAG	874
Qy	1147	CGTATTCGATGCAAGAGCATACAGCAAGAACTTCTAGATCTTTGACATTTGCTGATTAATC	1206
Db	875	CATATTCGATGCAAGAGCATACAGCAAGAACTTTAGATCTTTCACTTTGCTGATCTTAATC	934
Qy	1207	ATCAAAATTCAGGGGATACAGGTCGCTGCATGTTGACGCCATCAGGAAGAGCCTAAAA	1266
Db	935	ATCAAAATTCAGGACACAGCGTACTTCATGTTGCTGCCATCAGGAAGAGCCTAAAA	994
Qy	1267	TTGTAGTGTCCCTTTTAAACCAAGAGGCTAGACCTTCTGATCTGCATCCGATGGAAGAA	1326
Db	995	TTATAGTGTCCCTTTTAAACCAAGAGGCTAGACCTTCTGATCTGCATCCGATGGAAGAA	1054
Qy	1327	AAGCACTTCAAAATCGCCAAAGAGGCTACTAGGCTTTGTGGATTTTCAGTAAGTCTCCGGAG	1386
Db	1055	AAGCACTTCAAAATTCGTAAGAGGCTCACTAGGCTTTGATATTTTACCAAGTCTACAGAG	1114
Qy	1387	AAGGAAATCTGCTTCGAATGATCGGTTATGCATTTGAGATTTCTGGAGCAGCAGAAAGAA	1446
Db	1115	AAGGAAATCTGCTTCAAGAGGATCGGTTATGCATTTGAGATTTCTGGAGCAGCAGAAAGAA	1174
Qy	1447	GAGACCTCTGCTAGGAGAAGCTTCTGATCTCTTGTCTATGGCAGGCGATGATTTGGCTGA	1506
Db	1175	GAGATCCACTACTAGGAGAAGCTTCATTAATCTCTTGTCTATGGCAGGCGATGATTTGGCTGA	1234
Qy	1507	TGAAGCTGTTATACCTTGAATAAGATGTGGCTTAAACTCCTTTTCCAAATGGAAG	1566

Db	1235	TGAAGCTGTTATACCTTGAATAATAGAGTTGGCTGGCTAAACTCCTTTTCCCATGGAAG	1294
Qy	1567	CTAAAGTTGCAATGGACATTGCTCAAGTTGATGGCACTTCTGAGTGTCCCACTGGCTAGCA	1626
Db	1295	CAAAAGTTGCAATGGACATTGCACAAGTTGATGGCACTCTCAANTTACCCCTGGCTAGCA	1354
Qy	1627	TCGGCAAAAAGATGGCTAATGCACAGAGACAAACAGTAGATTGGAACGAGGCTCCTTTTCA	1686
Db	1355	TGAGGAAAGAAGATAGCTGTATGCACAGAGACAAACAGTGGATTTGAACGAGGCTCCTTTTCA	1414
Qy	1687	AGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTCTAGAACTTGGAA	1746
Db	1415	AGATGAAGAAGAGCACTTGAATCGGCTTAGGGCTCTCTAGAACTGTGGAACTTGGAA	1474
Qy	1747	AACCGTCTTTTCCACGCTTGTTCCAGAAGTTCTTAAATAAGATCATGGATGCTGATCACTTGT	1806
Db	1475	AACGGTTCTTTTCCACGCTTGTTCCAGAAGTTCTTAAATAAGATCATGGATGCTGATCACTTGT	1534
Qy	1807	CTGATAGAGCTTACATGGGGAATGATACGGCAGAGAGCGGTCAACTGAAGAAGCAAGGT	1866
Db	1535	CTGATAGAGCTTACATGGGGAATGATACAGTAGAAGACGCTCAACTGAAGAAGCAAGGT	1594
Qy	1867	ACATGGAACCTTCAAGAAATCTGACTAAAGCAATTCACCTGAGGATAAAGAAGCAATATGATA	1926
Db	1595	ACATGGAACCTTCAAGAAATTTTGTCTAAGCAATTCACGGAGGATAAAGAAGCAATTTGCTA	1654
Qy	1927	AGACTAACACATCTCCTCATCTTGTTCTCTACATCTAAGGAGTAGATAAGGCCCAATA	1986
Db	1655	AGACT---AACATGTCTCATCTTGTTCTCTACATCTAAGGAGTAGATAAGGCCCAATA	1711
Qy	1987	AGCTCCCTTTTAGGAAATAG	2006
Db	1712	ATCTCCCATTTTAGGAAATAG	1731

RESULT 4	
AAA97229	
ID	AAA97229 standard; cDNA; 2299 BP.
XX	
XX	AAA97229;
XX	
DT	25-JAN-2001 (first entry)
XX	
DE	B. vulgaris NIM1 homologue coding sequence SEQ ID NO: 63.
XX	
KW	Systemic acquired resistance; SAR; signal transduction cascade;
KW	disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW	potato; ss.
XX	
XX	Beta vulgaris.
OS	
XX	
PH	Key
FT	Location/Qualifiers
FT	113..1927
FT	/*tag= a
FT	/product= "NIM1 homologue"
FT	/trans_except= (pos:1877..1882aa;Ser)
XX	
PN	WO200053762-A2.
XX	
PD	14-SEP-2000.
XX	
PF	07-MAR-2000; 2000WO-EP01978.
XX	
PR	09-MAR-1999; 99US-0265149.
XX	
XX	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX	
XX	Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
PI	
XX	
XX	WPI; 2000-594322/56.
DR	P-PSDB: AAB27324
DR	

xx Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIMI gene -
xx
PS
xx Claim 3: Page 127-130; 152pp; English.
xx
CC The present invention is concerned with the isolation of NIMI homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIMI is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC gene and protein can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize.
xx
SQ Sequence 2299 BP; 644 A; 483 C; 510 G; 662 T; 0 other;
Query Match 36.0%; Score 781.2; DB 21; Length 2299;
Best Local Similarity 67.3%; Pred. No. 3.1e-201;
Matches 1186; Conservative 0; Mismatches 528; Indels 48; Gaps 4;
QY 247 ATAGTAGGACTGGTTTCTTGATTCGAAATGACATCAGCGAAGCAGTAGTATGCTGCA 306
DB 144 ATTCTGCGACCGTTTCTCGGATTCGAAAGACATCAGCATGCGCATGCTGCTGG 203
QY 307 TCGCGCGCGCATGACTGAAATTTTCTCGCGGAGA-----CTTGCGCGCGCG 354
DB 204 TCGCGCGCAACAACATACAAACACCGCGCGCAAAACCTCTCTCTTACTCCCG 263
QY 355 AGATCACTTCACGAAACGGCTATCGGAACACTGGAATCTATCTCGATGC-----GT 408
DB 264 ACGCGCGCGCTTCTCGCGCTCTCTGAAACCTCGACTCGCTTTTCCAAACCTCGCTTT 323
QY 409 CTTTTCGGGAGTTGACTACTCTCGCGAGCTAAAGCTGTGTTTCGGCCCGCTGTAAGG 468
DB 324 CTCTCTCGGACTCGGACTCTTTCGCGACGCTAAATCTGCTGTTCCGGTGATTCGCGTG 383
QY 469 AAATTCGCGTGACCGGTCATTTTGTGCGCGAGAGTCGGTTCCTTAAAGAAATTTGTTCT 528
DB 384 AAGTCGCGCTTCTCGGTGTGTTCTCTCGTCTCGGAGCTCGTCTTTCGCTCGCGTTTG 443
QY 529 CGGTAAGAGGAGAGAGATAGTAGTAAGTGAATGAGGAGGTGATGAAGAGC--- 585
DB 444 CTTTGAAG 503
QY 586 -----ATGAGGTGAGCTATGATGCTGTAATGAGTGTGATTTGGCTTATT 627
DB 504 AGGATTTAGCTGGTGATTTTGAGGTTGGATTTGATTCGGTTGTTCGGTTTATGTTATT 563
QY 628 TGTATAGTGTAAAGTTAGCGCTTCAACCTAAAGATGTGTGTGTTGTGTTGGACAATGACT 687
DB 564 TGTATAGTGTAAAGTTAGCAATTTGCTAGAGAAATTTGCTGTTGTTGTTGATGAGGAT 623
QY 688 GCCTCATGTGGCTGTAGCGGACGCTGCGCATCTCGTGTGAGTGTGTTTGTACACATCAT 747
DB 624 GCTCTCATGAAGCTTGTGCGTCTGCTGTTGATTTGTTGTGAGGTTCTCTATTTGCTC 693
QY 748 TTACTTTTCAGATCTCTGAAATTTGGTTGACAAAGTTTCAGAGACACCTACTGGATATTTTG 807
DB 684 ACAATTCGAGATTTGCGAATTTGTTTCGCTTTATCAGAGGACCTACTGGATATTTCTTG 743
QY 808 ACAAACTCGCAGCAGCATGTATGATGTTTATCTGTTGTTGTTGTTGTTGTTGTTGTTG 867
DB 744 ACAAGATTGACAGATGACGTTCTAGTAGTGTATCTGCTGCTGAGATGTGTGGAATG 803
QY 868 CATCGGAGAGATTGCTTCAAGCTGCATTGAGATTATTGTCAAGTCTAATGTTGATATCA 927

DB 804 CGTGTGACGGATTGCTGGCAAGGTGTATTGACAAGATTGTGAGTCCGATATTGACGTAA 863
QY 928 TAACCCCTTGATAAAGCCTTGCTCATGACATTGTAAACAAATTTACTGATTTCAGAGCGG 987
DB 864 CCACCATTTGATAAATTCCTTCCGCCAGAAATGTTGTGAACACAGATAATCGACACGGAAAG 923
QY 988 AACTTGGTCTTAAAGGGCCTGAAAGCAACGGTTTTCTCTGATAAACAATGTTAAAGAGTAC 1047
DB 924 AACTTGGTCTTACTGAACCTCGGCGTGTGAGTTTCTCTGATAAGCATGTGAAGAGATAAC 983
QY 1048 APAGGGCAATGGATTCTGATGATGTTGAATTACTACAAATGTTCTTAAGAGAGGGGCATA 1107
DB 984 ACAGAGCTTTTGAATCCGATGATGATGAGTTAGTCAGAAATGCTTTTAAAGAGCGCCATA 1043
QY 1108 CTACCTTAGATGATGATATGCTCTCCATTTATGCTGTAGCGTATTGCGATGCAAAAGACTA 1167
DB 1044 CAATCTTAGATGATGATATGCCCTTCACTAATGCTGTGGACATTTGATGCTTGTAAACCA 1103
QY 1168 CAGCAGAACTTCTAGATCTTGCACCTTGTCTGATATTAATCATCAAAATTCAGGGGATACA 1227
DB 1104 CCAGGAGCTTCTTGAGCTTGGGCTTGCAGATGTTAATCTTAGAAATCTAAGGGGTCA 1163
QY 1228 CGTGTCTCATGTTGCGCCATGAGGAAGAGCCTAAATTTGTAGTCTCCCTTTTAACCA 1287
DB 1164 CTGTCTACATGTGCGACCCATGAGAAAGAGCCTAAGATAAATTTGTATCTTGTAAACCA 1223
QY 1288 AAGAGCTTAGACCTTCTGATCTGACATCCGATCGGATGGAAGAAAGACACTTCAATCCCAAGA 1347
DB 1224 AGGAGCCCTCCGCTCTGATATAACATCAGATGATAAAGAGCACTGCAGATAGCAAGA 1283
QY 1348 GGCTCAGTGGGCTTGTGATTTAGTAAAGTCTCGGAGGAAGGAAATCTGCTTCGATG 1407
DB 1284 GACTAACAAAAAGCTGTGAGCTTCTATAAACTACAGAAACAAAGAAAAAGATGCACCAAGG 1343
QY 1408 ATCGGTTATGATTCAGATTCGAGGACGAGCAAGAGAGAGAGCCCTCTGCTAGGAGAAG 1467
DB 1344 ATCGGTTGCTGATTTGAAATCTGAGCAAGCTGGAAGAGAGAGCACTTGTCTAGAGAG 1403
QY 1468 CTTCTGTATCTCTGCTATGCGAGCGATGATTTGCGTATGAAAGCTGTTATACCTTGAAA 1527
DB 1404 GTTCTGTTCTCTTCAAGGCGAGGATGATCTGCGTATGAAGCTATTATATCTTGAAA 1463
QY 1528 ATAGAGTTGGCTGGCTAACTCTTTTCCAAATGGAAGCTAAAGTTGCAATGGACATG 1587
DB 1464 ATAGAGTTGCACTTCTCGGTGCTCTTTCCAAATGGAAGCGAAAGCTGCTATGATATG 1523
QY 1588 CTCAGTTGATGGCACTTCTGAGTTCCCACTGGCTAGCATCGGCAAAAGATGGCTAATG 1647
DB 1524 CTCAGTTGAGCGAAGCTTCTGAAATTCACATTGTC-----AAAGATATAGCTGATG 1574
QY 1648 CACAGAGCAACAGTAGATTGTAACAGGCTCCCTTTCAAGATAAAGAGGAGCACTTGA 1707
DB 1575 CACGAAGAAATCGGTGGACTTGAATGAGGCTCCCTTTTATATGAAGAGGAGCACTTGC 1634
QY 1708 ATCGGCTTAGACACTCTCTAGAACTGTAGAACTTGGAAAAGCGCTTTTCCAGCTTCTT 1767
DB 1635 AGAGATGAAGCACTGTCTAAACTGTTGAGCTTGGCAAGCGTTTCTTTCCAGCTCTCT 1694
QY 1768 CAGAAAGTTCTAAATAGATCATGGATGCTGATGACTTGTCTGAGATAGCTTACATGGGA 1827
DB 1695 CCGATGTTCTTAATAGATTTATGACGCGGAGATCTATCACAGCTTGCATTTTAGGAA 1754
QY 1828 ATGATACGGCAGAGAGCGCTCAACTGGAAGCAAGGATACATGGAAGCTTCAAGAAATTC 1887
DB 1755 AAGATACTCCAGAGGAAGCGCAAGAGAGAGAAAAACGATACCTTGAAGTGAAGACGCTT 1814
QY 1888 TGACTAAAGCACTTCTAGGATTAAGAGAAATATGATAAGACTAAACAACATCTCCTCAT 1947
DB 1815 TAACTAAGGCTTTTACAGAGGACAAAGAGAGTTTGACCGCTTACATATATCATCATCGT 1874
QY 1948 CTTGTTCTCTACATCTAAGGG 1969


```
Db 1875 CGTCGTCGCTGACTCCAATGGG 1896
RESULT 5
AAA97211
ID AAA97211 standard; DNA; 659 BP.
XX
AC AAA97211;
XX
XX 25-JAN-2001 (first entry)
XX
DE N. tabacum NIM1 homologue coding sequence SEQ ID NO: 29.
XX
XX Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW potato; ds.
XX
XX Nicotiana tabacum.
OS
XX
XX key Location/Qualifiers
FH 1..657
CDS /*tag= a
FT /product= "NIM1 homologue"
FT /partial
FT
XX WO200053762-A2.
XX
XX 14-SEP-2000.
XX
XX 07-MAR-2000; 2000WO-EP01978.
XX
XX 09-MAR-1999; 99US-0265149.
XX
XX (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX WPI; 2000-594322/56.
XX P-PSDB; AAB27308.
XX
XX Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIM1 gene -
XX
XX Claim 3; Page 102-103; 152pp; English.
XX
XX The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC gene and protein can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize.
XX
XX Sequence 659 BP; 200 A; 124 C; 153 G; 182 T; 0 other;
XX
XX Query Match 28.6%; Score 620.6; DB 21; Length 659;
XX Best Local Similarity 96.4%; Pred. No. 5.8e-158;
XX Matches 635; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
XX 891 TGCATTGAGATTATTGTCAGTCTAATGTTGATATCATACACCTTGTATAAGCCCTTGCCCT 950
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 TGCATGAGATTATTGTCAGTCTAATGTTGATATCATACACCTTGTATAAGCCCTTGCCCT 60
XX
XX 951 CATGACATTGTAACAAATTTACTGATTCACGAGCGGAACCTTGGTCTACAGGGCCTGAA 1010
```

```
Db 61 CATGACATTGTAACAAATTTACTGATTCACGAGCAGAACTTGGTCTACAGGGCCTGAA 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1011 AGCAACGGTTTTCTTGATAAACATGTTAAGAGGATACATAGGCGATTGGATTCTGATGAT 1070
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 121 AGCAATGGTTTTCTTGATAAACATGTTAAGAGGATACATAGGCGATTAGATTCTGATGAT 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1071 GTTGAATTTACTACAATGTTGCTAAGAGAGGGGCATCTACTACCTAGATGATCATATGCT 1130
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 181 GTTGAATTTACTCGAGATGTTGCTAAGAGAGGGGCATCTACTACCTAGATGATCATATGCT 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1131 CTCCATTATGCTGATGCGATTTGCGATGCAAGACTACAGCAGAACTTCTAGATCTTGCA 1190
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 241 CTCCACTATGCTGTAGCATATGCGATGCAAGACTACAGCAGAACTTCTAGATCTTGCA 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1191 CTTGCTGATATTATCATCAAAATTCAGGGGATACACGCTGCTGCATGTTTGCAGCCATG 1250
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 301 CTTGCTGATGTTAATCATCAAAATTCAGAGGATACACAGTCTGCATGTTGCAGCCATG 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1251 AGGAAAGACCTTAAATTTAGTGTCCCTTTTAAACCAAGAGGCTAGACCTTCTGATCTG 1310
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 361 AGGAAAGACCTTAAATTTAGTGTCCCTTTTAAACCAAGAGGCTAGACCTTCTGATCTG 420
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1311 ACATCCGATGGAAGAAAGCACTTCAAAATTCGCCAAGAGGCTCAGCTAGCTTGTGGATTTC 1370
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 421 ACATCCGATGCGAGAAAGCACTTCAAAATTCGCCAAGAGGCTCAGCTAGCTTGTGGATTTC 480
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1371 AGTAAAGTCTCCGGAGGAGGAAATCTGCTTGAATGATCGGTTATGCAATTTGAGATTCTG 1430
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 481 ACTAAGTCTCCAGAGGAGGAAATCTGCTTGAAGAGTCCGTTATGCAATTTGAGATTCTG 540
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1431 GAGCAAGCAGAAAGAGACCCCTCTGCTAGGAGAGGCTTCTGTATCTTCTGCTATGGCA 1490
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 541 GAGCAAGCAGAAAGAGAGATCCACTGCTAGGAGAGGCTTCTGTATCTTCTGCTATGGCG 600
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1491 GCGGATGATTTGCGTATGAAGCTGTTATACCTTGAATAGATTGGCTGGCTAAACT 1549
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 601 GCGGATGATTTGCGTATGAAGCTGTTATACCTTGAATAGATTGGCTGGCTAAACT 659
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
RESULT 6
AAC37765
ID AAC37765 standard; DNA; 2024 BP.
XX
AC AAC37765;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 18587.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 23-MAR-1999; 99US-0123548.
XX 29-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127482.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
```

PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141187.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142330.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.

[illegible]

```

XX  NPRI gene: acquired resistance; disease; plant pathogens; bacteria;
KW  mycoplasma; fungi; insects; nematodes; viruses; viroids;
KW  transgenic; ds.
XX  Arabidopsis thaliana.
OS
PH  Key Location/Qualifiers
FT  CDS 93..1874
      /tag= a
      /product= acquired resistance protein
      /note= NPRI gene
XX
PN  WO9806748-A1.
XX
XX  19-FEB-1998.
XX
XX  08-AUG-1997; 97WO-US13994.
XX
XX  16-MAY-1997; 97US-0046769.
PR  09-AUG-1996; 96US-0023851.
PR  10-JAN-1997; 97US-0035166.
XX
XX  (GEHO ) GEN HOSPITAL CORP.
PA  (UYDU-) UNIV DUKE.
XX
XX  Ausubel FM, Cao H, Dong X, Glazebrook J;
PI  WPT; 1998-159458/14.
XX  P-PSDB; AAW46940.
DR
XX
XX  New isolated plant acquired resistance polypeptide gene - useful
PT  for, e.g. producing plants with increased resistance to pathogens
PT  such as bacteria
XX
XX  Claim 9; Fig 5; 127pp; English.
PS
XX
CC  The sequence is that of the acquired resistance gene NPRI1. It may be
CC  used in the production of transgenic cells which can produce the encoded
CC  acquired resistance protein. Such transgenic plants' cells are
CC  useful in the production of plants having an increased level
CC  of resistance against disease caused by plant pathogens, e.g.
CC  bacteria, mycoplasmas, fungi, insects, nematodes, viruses,
CC  and viroids.
XX
XX  Sequence 2104 BP; 606 A; 431 C; 482 G; 585 T; 0 other;
SQ
      Query Match 26.6%; Score 578.4; DB 19; Length 2104;
      Best Local Similarity 62.8%; Pred. No. 2.8e-146;
      Matches 982; Conservative 0; Mismatches 546; Indels 36; Gaps 4;
QY  415 CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCGGCCCGCTGTAAGGAATTC 474
      || || || || || || || || || || || || || || || || || || || || || ||
DB  268 CGCCGGATGATTTCTACGCGACGCTAAGCTTGTCTCTCCGAC---GGCCGGGAAGTTT 324
QY  475 CGGTGCACCGGTGCATTTTTCGCGGAGGAGTCCGTTCTTTAAGAAATTTGCTTCGCGGTA 534
      || || || || || || || || || || || || || || || || || || || || || ||
DB  325 CTTTCCACCGGTGGTTTGTACGCGAAGACTCTTTCTTCAAGAGCGCTTTAGCCGCCG 384
QY  535 AAAAGGAGGAAGAAATAGTAGT-----AAGGTGGAATTTGAAGAGGTGA 576
      || || || || || || || || || || || || || || || || || || || || || ||
DB  385 CTAAGAGGAGGAAGAACTCCAAACACCGCCGCGCTGAAGCTCGAGCTTAAGGAGATTG 444
QY  577 TGAAGAGCATGAGGTGAGCTATGCTGTAAATGAGTGTATGGCTTATTTGTATAGTG 636
      || || || || || || || || || || || || || || || || || || || || || ||
DB  445 CCAAGGATTACGAATCGGTTTCGATTCGGTGTGACTGTTTGGCTTATGTTTACAGCA 504
QY  637 GTAAAGTTAGGCTTCACCTAAAGATGTGTGTTTGTGTGGCAATGACTGCTCTCATG 696
      || || || || || || || || || || || || || || || || || || || || || ||
DB  505 GCAGAGTGAGACCGCCGCTTAAGAGGTTTCTGAATGCGCAGAGAAATTCGTGCCACG 564
QY  697 TGGCTGTAGGCCAGCTGTGGCATTCCTCGTTGAGGTTTGTACACATCATTTACCTTC 756
      || || || || || || || || || || || || || || || || || || || || || ||

```

```

Db 565 TGGCTTGGCCGGCGCGGTGGATTTTCATGTTGGAGGTTCTCTATTGGCTTTCATCTTCA 624
QY 757 AGATCTCTGAATTTGGTTGACAAGTTTTCAGAGACACCTACTCGATATTCTTTGACAAAAC 816
      || || || || || || || || || || || || || || || || || || || || || ||
Db 625 AGATCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 684
QY 817 CAGCAGACGATGAATGATGTTTATCTGTGCAACATTTTGGTAAAGCATGCGGAGA 876
      || || || || || || || || || || || || || || || || || || || || || ||
Db 685 TTATAGAGGACACATTTGGTTTAACTCAAGCTTGTAAATATATGTTGTTAAAGCTTGTATGA 744
QY 877 GATTGCTTTCAAGCTGATTTGAGATTTTCAAGTCTAAATGTTGATATCATTAACCCCTTG 936
      || || || || || || || || || || || || || || || || || || || || || ||
Db 745 AGCTATTGGATAGATGTAAGAGATTTTGTCAAGTCTAAATGATAGATATGTTAGTCTTG 804
QY 937 ATAAAGCCTTGGCTCATGACATTTGAAAACAAATTAATTAATTAATTAATTAATTAATTA 996
      || || || || || || || || || || || || || || || || || || || || || ||
Db 805 AAAAGTCAATGGCGGAAGAGCTTGTAAAGAGATAATTTGATAGAGGTAAGAGCTTGGTT 864
QY 997 TACAAGGCGCTGAAAGCAACCGTTTTCCTGTATAACATGTTTAAAGAGATACATAGGGCAT 1056
      || || || || || || || || || || || || || || || || || || || || || ||
Db 865 TGGAGGTACCTAAAGTAA-----AGAAAACATGCTCTCGAATGTACATAAAGGCAC 912
QY 1057 TGGATTCGTGATGATGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1116
      || || || || || || || || || || || || || || || || || || || || || ||
Db 913 TTGACTCGGATGATATGAGTTAGTCAAGTTTGTCTTAAAGAGGATCACACCAATCTAG 972
QY 1117 ATGATGCAATGCTCTCCATTAATGCTGTAGGTTTTCGATGCAAGAGACTACAGCAGAAC 1176
      || || || || || || || || || || || || || || || || || || || || || ||
Db 973 ATGATGCGTGCTCTTTCATTTGCTGTGCTGTTGCTGCTGTTGCTGCTGTTGCTGCTGCT 1032
QY 1177 TTCTAGATCTTGCACCTTGTGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1236
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1033 TTTTAAACCTTCATCTTCCGATGTCAACCATAGGAATCCGAGGGGATATACGGTGTTC 1092
QY 1237 ATGTTGACCCATGAGGAAGAGCCTAAATTTAGTTAGTGTCCCTTTTAAACCAAGAGGCTA 1296
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1093 ATGTTTGTCTCGATGCGGAAGAGGCCACCAATTTGATATCTCTCTTGGAAAAGGTGCAA 1152
QY 1297 GACCTTCTCATCTGACATCCGATGGAAGAAAAGACACTTCAAAATCGCCAGAGGCTCACTA 1356
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1153 GTGCATCAGAACCACTTTTGAAGGTAGAACCGCACTCATGATCCCAAAACAGCCACTA 1212
QY 1357 GCGTTGTGGAATTCAGTAAAGTCTCCGGAGGAAGAAAATCTGCTTCGAATGATCGGTTAT 1416
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1213 TGGCGGTTGAATGTAATAATATCCGGAGCAATGCAAGCAATCTCTCAAGGCCGACTAT 1272
QY 1417 GCATTGAGATTTCTGGAGCAAGCAGAAAGAGACCCCTCTGCTAGGAGAGCTTCTGTAT 1476
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1273 GTGTAGAAATACCTAGAGCAAGAGAACAAACAGAGAACAAATTCCTAGAGATGTTCTCCCT 1332
QY 1477 CTCTTGCTATGCGAGCGGATGATTTTCGCTATGAAGCTGTTTATACCTTGAATAATAGATTG 1536
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1333 CTTTTCAGTGGCGCGGATGAATTCAGATGACGCTGCTCGATCTTGAATAATAGATTG 1392
QY 1537 GCGTGGCTAAACTCCCTTTTCCAAATGGAAGCTTAAAGTTGCAATGGACATGCTCAAGTTG 1596
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1393 CACTTCTCAACGCTCTTTTCCAAAGGAGCACAAGCTGCAATGGAGATCGCCGAAATGA 1452
QY 1597 ATGGCACTTCTGAGTTCCCACTGGCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA 1653
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1453 AGGGAACATGTGAGTTTCATAGTAGCTAGCTAGCTCGAGCTCGACCTGCTGCTGATGAGA 1512
QY 1654 GGACAAACAGTATGATTTGAACGAGGCTCCCTTTCAAGATAAAGAGGAGCACTTGAATCGGC 1713
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1513 GAACATCACCGGTTGTAAGATAGCACCTTTTCAAGATCTCTAGAAGAGCATCAAGTAGAC 1572
QY 1714 TTAGACACTCTCTAGAACTGTAGAATCTTGGAAAACGCTTCTTTCCAGCTTGTTCAGAG 1773
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1573 TAAAGCGCTTCTTAAACCGGTGGAACCTCGGAAACGATTTCTCCCGGCTGTCGGGAG 1632
QY 1774 TTCTAAATTAAGATCATGATGCTGCTGAGATGCTTCTGAGATAGCTTACATGCGGAATGATA 1833
      || || || || || || || || || || || || || || || || || || || || || ||
Db 1633 TGCTCGACCAAGATTATGAATCTGTGAGGACTTGACTCAACTGCTTGGCGAGAGAGCACA 1692

```



```
QY 1477 CTCCTTGCTATGCGAGCGCATGATTTTTCGCTATGTAAGCTGTTTATACCTTGAAAATAGAGTTG 1536
Db 1283 CTTTTCGCTAGTGGCGCGCATGAATTTGAAGATGAGCGTCTCGATCTTGAAAATAGAGTTG 1342
QY 1537 GCGTGGCTAAACTCCTTTTTCCTCAATGGAAGCTGAAGTTTGAATGACATTTGCTCAAGTTG 1596
Db 1343 CACTTGGCTCAAGCTCTTTTTCCTCAAGGGAAGCACAAGCTGCAATGGAGATCCCGAAATGA 1402
QY 1597 ATGGCACTTCTGAGTCCCACTGGCTAGCATCG---GCCAAAAGATGGCTAATGCACAGA 1653
Db 1403 AGGGAACATGTGAGTTCATAGTACTAGACCTCGAGCCTCGACCGTCTCACTGGTACGAGA 1462
QY 1654 GCACACACAGTATGATTTGAACGAGGCTCCTTCAAGATAAAAGAGAGCAGCTTGAATCGGC 1713
Db 1463 GAACATCACCGGGGTGAAGATAGACACCTTTTCAGATCCTAAGAGAGCATCAAAAGTAGAC 1522
QY 1714 TTAGAGCACTCTCTAGAACTGTAGAACTTGGAACACGCTTCTTCCAGGTTTGTTCAGAAAG 1773
Db 1523 TAAAGCGCTTCTTAAACCGTGAAGCTCGGAAACGATTTCTCCCGGCTGTTTCGGCAG 1582
QY 1774 TTCTAAATAAGATCATGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGGAATGATA 1833
Db 1583 TGCTCGACACAGATTATGAAGTGTGAGGACTTGACTCAACTGGCTTGCGGGAAGACGACGA 1642
QY 1834 CGGCAGAAAGCGTCAACTGAAGAAGCAAAAGGTACATGGAACCTTCAAGAAATTTCTGACTA 1893
Db 1643 CTGCTGAGAAACGACTACAAAAGAAGCAAAAGGTACATGGAATGGAATACAAAGACACTAAGA 1702
QY 1894 AAGCATTTCACTGAGGATAAAGAAAGATATGATAAGACTTAACAACATCTCCTCATCTTGT 1953
Db 1703 AGGCCTTTAGTCAGGCAATTTTGGAAATTTAGGAAATTTGTCCCTGACAGATTGCGACTTCT 1762
QY 1954 CTCCT 1957
Db 1763 CCAC 1766

RESULT 9
AAV46275
ID AAV46275 standard; cDNA; 2011 BP.
XX
AC AAV46275;
XX
DT 16-OCT-1998 (first entry)
XX
DE A. thaliana NIM-1 cDNA variant #1.
XX
KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
OS Arabidopsis thaliana.
OS Synthetic.
XX
FH Location/Qualifiers
FT 43..1824
FT CDS
FT /tag= a
FT /product= NIM-1
FT /note= "variant"
FT 205..207
FT mutation
FT /tag= b
FT /note= "wild type TCC is replaced by GCC"
FT 217..219
FT mutation
FT /tag= c
FT /note= "wild type TCG is replaced by GCG"
XX
PN W0829537-A2.
XX
PD 09-JUL-1998.
XX
PF 23-DEC-1997; 97WO-EP07253.
XX
```

```
PR 10-JAN-1997; 97US-0035024.
PR 27-DEC-1996; 96US-0034378.
XX
XX (NOVS ) NOVARTIS AG.
XX
PI Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;
DR WPI; 1998-388119/33.
DR P-PSDB; AAW64436.
XX
PT Protection of immunomodulated plants against pathogens - comprises
PT applying microbicide to provide increase in resistance
XX
XX Claim 11; Page 116-120; 164pp; English.
XX
XX This sequence encodes a variant NIM-1 protein from Arabidopsis
CC thaliana. This protein is used in a method resulting in the protection of
CC an immunomodulated plant having a first level of resistance and involves
CC treatment with at least 1 microbicide that confers a second level of
CC resistance, such that the plants have a third level of resistance greater
CC than the sum of the first two levels. The method can be applied to a wide
CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
CC against viruses, fungi, bacteria, insects and nematodes. The method
CC provides a high level of resistance and allows a reduction in the amount
CC of microbicide used. Since the process involves two different methods of
CC protection, it is unlikely that the pathogen will develop resistance to
CC the treatment.
XX
SQ Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;

Query Match 26.6%; Score 576.8; DB 19; Length 2011;
Best Local Similarity 62.7%; Pred. No. 7.3e-146;
Matches 981; Conservative 0; Mismatches 547; Indels 36; Gaps 4;

QY 415 CGAGTTTGACTACTTCGCGGAGCTAAGCTTCTGCTTCGCGCGCTGTAAAGAAATTC 474
Db 218 CGCGGATGATTTTCAGCGGAGCTAAGCTTGTCTCTCCGAC---GGCGGGAAGTTT 274
QY 475 CGGTGCACCGGTGCATTTTTCGCGGAGGAGTCCGTTCTTTAAAGAAATTTGTTCTCGCGTA 534
Db 275 CTITCCACCGGTGGTTTTTGTGAGCGAGAGCTTTTCTTCAAGAGCGCTTTAGCGCGC 334
QY 535 AAAAGAGAGAATAGTAGT-----AAGTGGAAATGAAGGAGGTGA 576
Db 335 CTRAGAAGAGAGAAAGACTCCACAACACCCCGCGCTGAAGCTCGAGCTTAAGGAGATTG 394
QY 577 TGAAGAGCATGAGGTGAGCTATGATGCTCTAATGAGTGTATTGGCTTATTGTATAGTG 636
Db 395 CCAAGGATTAGAAAGTCGGTTTCGATTCGGTTGTGACTGTTTGGCTTATGTTACAGCA 454
QY 637 GTAAAGTTAGGCTTTCACCTAAAGATGTGTGTTGTGTTGGACAATGACTGCTCTCATG 696
Db 455 GCAGAGTGAGACCGCGCTTAAAGAGTCTTCTGAATGCGCAGACGAGAATTGCTGCACG 514
QY 697 TGGCTTTAGCCAGCTGTGCGCATTCCTGCTTGAAGTTTGTACACATCATTTACCTTTC 756
Db 515 TGGCTTGC CGCGCGGTGGATTTCATGTTGGAGGTCTCTATTTGGCTTTTCATCTTCA 574
QY 757 AGATCTCTGAATTTGTTGACAAGTTTCAGAGACACCTTACTGGATATTCTTGACAAAAGT 816
Db 575 AGATCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 634
QY 817 CAGCAGACGATGTAATGATGTTTTATCTGTTGCAACATTTGTGGTAAAGAGTGGCAGA 876
Db 635 TTATAGAGGACACATTTGGTTATACTCAAGCTTGCTAATATATGTTGGTAAAGCTTGTATGA 694
QY 877 GATTGCTTTCAGCTGCATTTGAGATTATTTGCAAGTCTAATGTTGATATCATACCTTTC 936
Db 695 AGCTATTGGATAGATGTAAGAGAGATTATTTGCAAGTCTAATGTTGATATGTTAGTCTTG 754
QY 937 ATAAAGCTTTCGCTCATGACATTTGTAACAAATTAATTAATTAATTAATTAATTAATTAAT 996
Db 755 AAAAGTCATTCGCGAAGAGCTTCTTTAAAGAGATAATTTGATAGACGTAAGAGCTTGGTT 814
```

```
QY 997 TACAAGGCGCTGAAGCAACGGTTTTTCCTGATAAACAATGTTAAGAGGATACATAGGCGAT 1056
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 815 TGGAGTAGCTAAAGTAA-----AGAAACATCTCTCGAATGTACATAAGGCAC 862

QY 1057 TGGATTCTTGATGATGTTGAATTACTACAATATTGCTAAGAGAGGGGATACACCCCTAG 1116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 863 TTGACTCGGATGATATTAGTTAGTCAAGTCTGTTTGAAGAGGATCACACCAATCTAG 922

QY 1117 ATGATGCATATGCTCTCCATATTGCTGTAGCTATTGGGATCGCAAGACTACAGCAGAAC 1176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 923 ATGATCGGTGCTCTCTTCATTTTCGTTGTCATATTGCAATGTGAAGACCGCAACAGATC 982

QY 1177 TTCTAGATCTTGCACTTGCTGATATTAAATCATCAAAATTCRAAGGGATACAGGTCCTGC 1236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 983 TTTTAAACTTGATCTTGCCGATGTCACCACTAGGAATCCGAGGGGATATACGGTGCCTC 1042

QY 1237 ATGTTGCACCCATGAGGAAGAGCCCTAAATTTGTAGTGTCCCTTTTAAACCAAGAGCTA 1296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1043 ATCTTGCTCGGATGCGGAAGGAGCCACAATTCATATCTATCTCTATTGGAAAAAGTGCAA 1102

QY 1297 GACCTTCTCATCTGACATCCGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1103 GTGCATCAAGAAGCACTTTGGAAGGTAGAACCCCACTCATGATCGCAAAACAAAGCCACTA 1162

QY 1357 GGCTTGTGATTTCTAGTAAGTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1163 TGGCGGTTGAATGTAATATATATCCCGGAGCAATGCAAGCATCTCTCAAGGCCCACTAT 1222

QY 1417 GCATTGAGATTTGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1223 GTGTAGAAATACTAGAGCAAGAAGACAAACAGAGAGACAAATTCCTAGAGATGTTCTCCCT 1282

QY 1477 CTCCTGCTATGCGAGGCGATGATTTGCGTATGAAGCTGTTATACCTTGAAATAGAGTTG 1536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1283 CTTTTCGATGCGGCGGCGGATGATTTGAAGATGACGCTGCTGATCTTGAAATAGAGTTG 1342

QY 1537 GCGTGGCTAAATCCCTTTTCCAAATGGAAGCTAAAGTTGCAATGACATGCTCAGTTG 1596
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1343 CACTTGCTCAAGCTCTTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1402

QY 1597 ATGGCACTTCTGAGTCCCACTGGCTAGCATCG---GCAAAAAGATGGCTAATGACACAGA 1653
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1403 AGGGAACATGTGAGTTTCATAGTACTAGCTCGAGCCTGACCGTCTCACTGGTAGAGA 1462

QY 1654 GCACAACAGTAGATTGAAGAGGCTCTTTTCAAGATAAAGAGGAGGAGGAGGAGGAGGAGG 1713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1463 GAACATCACCGGGTGTAAGATAGCACCTTTTCAGAAATCCTAGAAGAGCATCAAAGTAGAC 1522

QY 1714 TTAGAGCACTCTAGAACTGTAGAACTTGGAAAACGCTTCTTCCAGCTGTTTCAGAG 1773
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1523 TAAAGCGGTTCTTAAACCGTGGAACTCGGGAACGATTTCTCCCGCGCTGTTCGGCAG 1582

QY 1774 TTCTAAATAGATCATGATGCTGATGACTTGTCTGAGATAGCTTACATGCGGAATGATA 1833
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1583 TGCTGACCAGATTATGAAGTGTAGGACTTGAGCTCACTCACTGGCTTGGCGAGAGACGACA 1642

QY 1834 CGGCAAGAGCGCTCACTGAAGAGCAAGGTACATGGAACCTTCAAGAAATTTCTGACTA 1893
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1643 CTGCTGAGAAACGACTACAAAAAGCAAGGTACATGGAATACAAAGAGACACTAAAGA 1702

QY 1894 AAGCATTCCTCAGGATAAAGAGATATATGATAAGACTTAACACACTCTCCCTCATCTTTT 1953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1703 AGGCTTTAGTGAGGACAAATTTGGAATTAGGAAATTTGTCCTGTGACAGATTCGACTTCTT 1762

QY 1954 CCTC 1957
    |||
Db 1763 CCAC 1766
```

RESULT 10

AAV43661

ID AAV43661 standard; cDNA; 2011 BP.

XX AC AAV43661;
XX DT 29-SEP-1998 (first entry)
XX DE Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA.
XX KW Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;
XX KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;
XX KW constitutive immunity; agriculture; variant; ss.
XX OS Arabidopsis thaliana.
XX OS Synthetic.
XX FH Key
XX FT CDS Location/Qualifiers
FT FT /*tag= a
FT FT /product= "NIM1 protein variant 1"
FT FT 205..207
FT FT mutation /*tag= b
FT FT /note= "wild type TGC is replaced by GGC"
FT FT 217..219
FT FT /*tag= c
FT FT /note= "wild type TGC is replaced by GCG"
XX XX WO9826082-A1.
XX PN 18-JUN-1998.
XX PD 12-DEC-1997; 97WO-EP07012.
XX PF 20-JUN-1997; 97US-0880179.
XX PR 13-DEC-1996; 96US-0033177.
XX PR 27-DEC-1996; 96US-0034379.
XX PR 27-DEC-1996; 96US-0034382.
XX PR 10-JAN-1997; 97US-0034730.
XX PR 10-JAN-1997; 97US-0035021.
XX PR 10-JAN-1997; 97US-0035022.
XX XX (NOVS) NOVARTIS AG.
XX XX Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HV;
XX PI Uknes SJ;
XX XX WPI; 1998-348536/30.
XX DR P-PSDB; AAW61983.
XX PT Use of non-inducible immunity-1 gene - for transforming plants to
XX PS produce transgenic plants having a broad spectrum disease resistance
XX XX Claim 5; Pages 140-144; 205pp; English.
XX CC This cDNA encodes an altered form of the Arabidopsis thaliana non-
XX CC inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
XX CC AAV43665 represent variants of the NIM1 cDNA. The invention provides a
XX CC chimeric gene comprising a promoter active in plants operatively linked
XX CC to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
XX CC cells stably transformed with a recombinant vector comprising such a
XX CC chimeric gene have a broad spectrum of disease resistance. The altered
XX CC NIM1 proteins act as dominant-negative regulators of the systemic
XX CC acquired resistance (SAR) signal transduction pathway. The transgenic
XX CC plants transformed with an altered NIM1 gene exhibits constitutive SAR
XX CC expression which is higher in the transformed plants than in a wild-type
XX CC plant. The products can be used for producing plants with a broad
XX CC spectrum disease resistance. Overexpression of NIM1 mimics the effects
XX CC of inducer compounds that induce constitutive immunity (CIM) phenotype
XX CC in plants. The inventions can be used with plants such as rice, wheat,
XX CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
XX CC chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
XX CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
XX CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
XX CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry, tobacco,
XX CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,

14-SEP-2000.

07-MAR-2000; 2000WO-EF01978.

09-MAR-1999; 99US-0265149.

(NOVS) NOVARTIS AG.

(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Salmeron JM, Weislo LJ, Willits MG, Mengiste T;

WPI; 2000-594322/56.

P-PSDB; AAB27316.

Novel plant genes for enhancing systemic acquired resistance gene expression and broad spectrum disease resistance in plants, are homologues of Arabidopsis NIM1 gene -

Claim 3; Page 115; 152pp; English.

The present invention is concerned with the isolation of NIM1 homologues and their coding sequences from Arabidopsis thaliana, Brassica napus, Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The gene and protein can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, pelargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including Phytophthora parasitica and Peronospora tabacina, bacteria such as Pseudomonas syringae and P. tabaci, insects, including aphids and lepidoptera and nematodes such as Meloidiomyne incognita. In particular they can be used against disease organisms of maize.

Sequence 653 BP; 200 A; 124 C; 140 G; 187 T; 2 other;

Query Match	26.5%;	Score 575.4;	DB 21;	Length 653;
Best Local Similarity	92.3%;	Pred. No. le-145;		
Matches 603;	Conservative	2;	Mismatches 48;	Indels 0;
QY 897	GAGATTATTGTC	CAAGTCTA	AATGTTGATATCAT	AACCCCTTGATAAGGCTTGCCCTCATGAC 956
Db 1	GAKATTATTGTC	CAAGTCTA	AATGTTGATATCAT	AACCCCTTGATAAGTCTTGCCCTCATGAC 60
QY 957	ATTGTTAAACA	AAATCTACTG	ATTCACGAGCGGA	CTTGGCTTACAAGGGGCTGAAAGCAAC 1016
Db 61	ATCGTAAAA	CAAAATCACTG	ATTACGTCGCTGA	ACTTGGCTTACAAAGGGGCTGAAAGCAAT 120
QY 1017	GGTTTTCCCT	GATAAACATGTT	TAAGAGGATACAT	AGGCGATTGGATCTGATGATGTTGAA 1076
Db 121	GGTTTTCCCT	GATTAACATGTT	TAAGAGGATACAT	AGGCGATTGGACCTCTGATGATGTTGAG 180
QY 1077	TTACTACAA	ATGTTGCTT	AAGAGGGGCAT	ACTACCCCTAGATGATGATGCTGCCAT 1136
Db 181	TTACTAAG	ATGTTGCTT	TAAGAAGGGCAT	ACTACTCTCGATGATGATGCTCTCCAC 240
QY 1137	TATGCTGT	AGCCGATAT	TGCGATGCCA	AGACTACACAGCAACTCTAGATCTTGCACTTGGT 1196
Db 241	TATGCTGT	AGCATAT	TGGGATGCA	AAAGACTACACAGCAACTTTTAGATCTTTTCACCTTGGT 300
QY 1197	GATATTAA	TATCATCAAA	ATTCAAAGGGGAT	ACACGGTGTGTCATGTTGCAGCCATGAGGAA 1256
Db 301	GATGTTAA	TATCATCAAA	ATTCCTTAGAGG	ATACACGGTACTTCTATGTTGCTGCCATGAGGAAA 360
QY 1257	GAGCCTAA	AAATTTGATGT	GTCCCTTTT	TAAACCAAGAGGCTAGACCTTCTGATCTGCATCC 1316
Db 361	GAGCCTAA	AAATTTATAGT	GTCCCTTTT	TAAACCAAGAGGCTAGACCTTCTGATCTGCATCT 420
QY 1317	GATGGA	AAAAAGCACTT	CAAAATCGCA	AGAGGCTCACTAGGCTTGTGGATTTCACTAAG 1376
Db 421	GATGCA	AAAAAGCCAT	TTCAAATTTG	CTAAGAGGCTCACTAGGCTTGTGGATTTCACTAAG 480

XX										
SQ	Sequence	2040 BP;	501 A;	525 C;	553 G;	461 T;	0 other;			
	Query Match	25.9%;	Score 563.4;	DB 22;	Length 2040;					
	Best Local Similarity	64.3%;	Pred. No. 3.2e-142;							
	Matches	884;	Conservative 0;	Mismatches 476;	Indels 15;	Gaps 2;				
QY	580	AAGAGCATGAGGTGAGCTATGATGCTCTAATGAGTGATTTGGCTTATTGTTATAGTGGTA	639							
DB	356	AGGAGGTGGAGTGGGTAGAGGCGCTGGCGGTGGTGGCTCGACTACCTCTACAGCGGCC	415							
QY	640	AAGTTAGGCCCTTACCTAAAGATGTGTGTTTGTGTGGACAATGACTGCTCTCATGTGG	699							
DB	416	CGGTGCGGACCTGCCAAGCGCGTGCCTCTGCGTCGACGAGGACTGCGCCACGTCG	475							
QY	700	CTTGTAGGCCAGCTGTGGCATTTCTGGTTGAGGTTTGTGTACACATCATTTACCTTTTACA	759							
DB	476	GGTGCCACCCCGCTGCGTTCATGCGCAGAGTCCCTTTCCGCGGCTCCACCTTCCAGG	535							
QY	760	TCTCTGAATTGGTTGACAAGTTTTCAGAGACACCTACTGGATATTCTTTGACAAAACCTGCAG	819							
DB	536	TCGCCGAGCTCACCACCTCTTCACGCGCGTCTCTTGATGCTCTTGATAAGGTTGAAG	595							
QY	820	CAGACGATGTAATGATGTTTTATCTGTTGCCAAACATTTGTGTTAAAGCATGCGAGAGAT	879							
DB	596	TAGATAACCTTCTATTGATCTTATCTGTGCGCAACTTATGCAACAAATCTTGATGAAC	655							
QY	880	TGCTTTCAAGCTGCATTCAGATATTGTCAAGTCTAATGTTTGATATCATAAACCTTTGATA	939							
DB	656	TGCTTGAAGATGCTTGATATGTTAGTGTGCGGTCAAACTTGACATGTTACTTCTTGAGA	715							
QY	940	AAGCCTTGCCCTCATGACATTTGATAAAATAATTTACTGATTCACGAGCGGAACCTTGGTCTAC	999							
DB	716	AGTCATTGCCCTCCAGATGTTATCAAGCAGATATTGATGCAAGCCTTAAGCCTCGGATTAA	775							
QY	1000	AAGGCGCTGAAAGCAACGTTTTCTCGATAACATGTTAAGAGGATACATAGGCGATTGG	1059							
DB	776	TTTCACCAAGAAAACAAAGGATTCTCTAACAAACATGTGAGGAGGATACACAGAGCCCTTG	835							
QY	1060	ATTCGTGATGATGTGAATTTACTACAAATTTGCTTAAGAGAGGGGCATACCTAGCATG	1119							
DB	836	ACTCTGACCATGTAGAGCTAGCTAGGATGCTGCTCACTGAAGGACACACAAATCTTGATG	895							
QY	1120	ATGCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGCAAGACTACAGCAGAACTTC	1179							
DB	896	ATGCGTTTGCACTGCACCTACGCGTGCAGAACATTTGATCTCCAAATTTACACCGAGCTTT	955							
QY	1180	TAGATCTTGCACCTTGCTGATATTATCATCAAAATTTCAAGGGGATACAGGTGCTGCAATG	1239							
DB	956	TGGATCTCGCACCTTGCAATGTTAATCATAGAAAACCCCAAGAGGTTATCTGTTCTTCACA	1015							
QY	1240	TTGCAGCCATCAGGAAAGAGCCTAAATTTGATGTCCTCTTTTAACCAAGGAGCTAGAC	1299							
DB	1016	TTGCTCGGAGCGAAGAGAGCCTAAATTCATTTGCTCTCTTTTAACCAAGGGGCTCGAC	1075							
QY	1300	CTTCTGATCTGACATCCGATGGAAGAAAGACCTTCAAAATCGCCCAAGAGGCTCACTAGGC	1359							
DB	1076	CAGCAGATGTTACATTCGATGGGAGAAAGCGGTTCAAAATCTCAAAAAGACTAACAAC	1135							
QY	1360	TTGTGATTTTCAGTAAGTCTCCGGAGGAAGAAATCTGCTTTCGAATGATCGGTTATGCA	1419							
DB	1136	AAGGGGATTACTTTGGGTTTACCAGAAAGGAAACCTTCTCCAAAAGATAGGTTATGTA	1195							
QY	1420	TTGAGATCTCGAGCAAGCAGAAAGAGACCTCTGCTAGGAGAGAGCTTCTGTATCTC	1479							
DB	1196	TTGAAATTAATGAGCAAGCTGAAGAGAGGGACCCACAACCTCGGAGAGCATCATTTCTC	1255							
QY	1480	TTGCTATGCGAGCGGATGATTTGGCTATGAAGCTGTTATACCTTTGAAAATAGAGTTGGCC	1539							
DB	1256	TTGCAATGGCAGGTGAGAGTCTACGAGGAAGGTTGCTGTATCTTTGAAAACCGAGTTGCTT	1315							
QY	1540	TGGCTAAACTCGCTTTTTCGAATGGAGCTAAAGTTGCAATGGACATTCGCTCAAGTTGATG	1599							

DB	1316	TGGCAAGGATTATGTTTCCGATGGAGCAAGAGTAGCAATGGATATTTGCTCAAGTGGATG	1375
QY	1600	GCACCTTCTGAGTTCCTCACTGGCTAGCATCGCAAAAAGATGGCTAATGCACAGAGGACAA	1659
DB	1376	GAACTTTGGAATTTAACTGGTTCCTGGTGCNAATCCACCTCCTGAAAGACAACGGACAA	1435
QY	1660	CAGTAGATTGTAACGAGGCTCCTTTCAAGATAAAAAGAGAGACACTTTGAATCGGCTTAGAG	1719
DB	1436	CTGTTTGTCTAAATGAAAGTCTCTTTTCAATAAGAAAGAACACTTAGCTGGATGACAG	1495
QY	1720	CACCTCTAGAACTGTAGAACTTGGAAAACGCTTTTCCACGTTGTTCCAGAAGTTCTAA	1779
DB	1496	CACCTCTCAAAAACAGTGGAGCTCGGAAACGCTTTTCCCGGATGTTTCGACGTCGTCG	1555
QY	1780	ATAAGATCATGATGCTGATGACTTTGCTGTAGATAGCTTACATGGGGAATGATACGGCAG	1839
DB	1556	ACAAGATCATGATGATGA-----AAGTATCCCGTTTCCCTCGGAAGAGACAGTCCG	1609
QY	1840	AAGAGCGTCAACTGAAGAAAGCAAGGTACATGAACTTCAAGAAATTTCTGACTAAAGCAT	1899
DB	1610	CGGA-----GAAGAGGAAGAGGTTTCATGACCTGCAGGATGTTCTTCAGAAGGCAT	1660
QY	1900	TCACCTGAGGATAAAGAGAAATATGATAAGACTAACAAACATCTCCTCATCTTCTTC	1954
DB	1661	TCCACGAGGACAAGGAGGAGATGACAGTCTGGGGCTCTCTGCTCGTCGTCATC	1715

RESULT 13

AAA61047
ID AAA61047 standard; cDNA; 2194 BP.

XX AAA61047;

XX 12-OCT-2000 (first entry)

DE Rice putative negatively phytochrome regulated 1 (NPRI) gene #1.

XX Rice; negatively phytochrome regulated 1 gene; NPRI;
KW systemic acquired resistance; gene mapping; transgenic plant; ss.

XX Oryza sativa.

XX Key Location/Qualifiers

FT CDS 140..1876

FT /*tag= a

FT /product= "NPRI"

XX WO200028036-A2.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-US25953.

XX 05-NOV-1998; 98US-0107242.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Ramodu OO, Fang Y, Liu Z, Miao G, Odell JT;

XX WPI; 2000-451636/39.

XX P-PSDB; AAB09875.

XX Isolated nucleic acid fragments encoding an NPRI gene which can be used

XX to transform plants and provide disease resistance .

XX Claim 2; Page 29; 35pp; English.

XX The present sequence is a putative version of the rice negatively

CC phytochrome regulated 1 (NPRI) gene coding sequence. It was isolated by

CC screening a leaf cDNA library for those sequences which were

CC similar to the NPRI gene from Arabidopsis thaliana. The protein is

CC involved in systemic acquired resistance and this gene can be used to

CC create transgenic plants which are protected from pathogens. It can also

CC be used to find homologous sequences in other plants which have a similar
CC effect.

SQ Sequence 2194 BP; 510 A; 586 C; 617 G; 481 T; 0 other;

Query Match	25.7%	Score 558.6;	DB 21;	Length 2194;
Best Local Similarity	64.1%	Pred. No. 6.6e-141;		
Matches 881; Conservative	0;	Mismatches 479;	Indels 15;	Gaps 2;

QY 580 AAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTGTATTGGCTTATTGTATAGTGGA 639

Db
483 AGGAGGTGGAGGTTCGGGGTACGAGGCGGTGGGGTGGTGGTACCTACACCCCC

[illegible]

24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

[illegible]

QY /00 CTGTAGGCCAGCTGTGGCATTCCTGGTTTGAGGTTTGTACACATCATTTACCTTTCAGA 759

Db 603 GGTGCCACCCCGCGTTCATGGCGCAGTCTTTCGCGCCTCCACCTTCCAGG 662

QY 760 TCTCTGAATTGGTTGACAAAGTTTCAGAGACACCTACTGGATATTCCTTGACAAACTGCAG 819

Db 563 TCGCCGAGCTCACCACCTCTTCCAGCGGCTCTCCTTGATGTCCTTGATAAGGTTGAGG 722

QY 820 CAGACGATGTAATGATGGTTTTATCTGTTGCAACATTTGTGGTAAAGCATGCGAGAGAT 879

[illegible][illegible][illegible]

55 703 TGCCTGGAAAGATGCCCTTGAATAGGTAGTCCGGTCAAACCTTTGACATGATTACTCTTGAGA 842

QY 940 AAGCCTTGCCCTCATGACATTGTAAACAAATTACTGATTACGAGCGGAAC TTGGTCTAC 999

Db 843 AGTCAT^TTGCCTCCAGATGTTATCAAGCAGATTATTGATGCACGCCTAAGCCTCGGATTAA 902

QY 1000 AAGGCCCTGAAGCAACGGTTTCCCTGATAAACATGTTAAGAGGATACATAGGCATTGG 1055

Db 903 TTTCACCGAAACAAGGGATTTCCTAACAAACATGTGAGGAGGATACACAGAGCCCTTG 962

QY 1060 ATCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAGAGGGCCATATCTACCCCTACATC 1116

[illegible][illegible]

1179

52 1023 ATGCGTTTGGCAGCAGCAGCAGCGCTCGAACAATGTGACTCCAAAATACAAACCGAGCTTT 1082

QY 1180 TAGATCTGACATGCTGATATTAATCATCAAAATTC AAGGGATACACGGTGCTGCATG 1239

Db 1083 TGGATCTCGCACTTGCAGATGTTAATCATAGAAACCAAGAGGTTATACTGTCTTCACA 1142

QY 1240 TTGCAGCCATGAGGAAAGAGCCTAAATTTGTAGTGTCCTTTTAAACCAAGGAGCTAGAC 1299

Db 1143 TTGCTGCGAGCGAAGAGAGCCTAAAAATCATTTGCTCTCCCTTTTAACCAAGGGGGCTCGGC 1202

QV 1300 CTTCTGATCTGACATCCGATGGAGAAAGCACTTCATATCCCCCAACACCCCTCAGCTCCG 1350

pb
1202

120

5' TGGGATTCAGTAAAGTCTCCGAGGAAGAATACTGCTTCGAATGATCGGTATATGCA T419

1263 AAGGGGATTTACCTTGGGGTTACCGAAGGAAAACCTTCTCCAAAAGATAGGTTATGTA 1322

1420 TTGAGATTCTGGAGCAAGCAGAAAGAAGAGACCCCTCTGCTAGGAGAAGCTTCTGTATCTC
1479

Db 1323 TTGAAATACTGGAGCAAGCTGAAAGAAGGACCCACAACCTCGGAGAAGCATCAGTTTCTC 1382

QY 1480 TTGCTATGGCAGCGGATGATTTCGGTATGAAGCTGTTATACCTTGAAAAATAGAGTTGGCC 1539

[illegible]

Qy	1540	TGGCTAAACTCCCTTTTTCCTAATGGAAGCTAAAGTTGGCAATGGACATTCCTCAAGTTGATG	1599
Db	1443	TGGCGAGGATATGTTTTCCTCATGGGCAAGAGTAGCAATGGATATTGCTCAAGTTGGAT	1502
Qy	1600	GCACCTCTGAGTTCCCACTGGCTAGCATCGGCAAAAAGATGCTTAATGCACAGAGGACAA	1659
Db	1503	GAACCTTTGGGAATTTAACCTTGGGTTCTGGTGGCAATCCACCTCCTCAAAAGACAACGGACAA	1562
Qy	1660	CAGTAGATTTGAACGAGGCTCCTTTTCAAGATAAAAAGAGACACCTTGAATCGGCTTAGAG	1719
Db	1563	CTGTTGATCTAAATGAAGTCCTTTCATATAAGAAAGAACACTTACCTCGGATGACGG	1622
Qy	1720	CACCTCTAGAACTGTAGAACTTGGAAAACGGCTCTTTCACGTTGGTTCAGAAAGTTCTAA	1779
Db	1623	CACCTCTCAAAACAGCTGGAGCTCGGAAAACGGTTTTTCCGCGATGTTTCGAACCTGCTCG	1682
Qy	1780	ATAAGATCATGGATGCTGATGACTTCTCTGAGATAGCTTACATGGGAATGATACGGCAG	1839
Db	1683	ACAAAGATCATGGATGATGA -----ACCTGATCCCGGTTTCCCTCGGAAGAGACACGTCGG	1736
Qy	1840	AAGAGCGTCAACTTGAAGAAGCAAGATACATGGAACCTTCAAGAAATTCCTGACTAAAGCAT	1899
Db	1737	CGGA -----GAAGAGGAAGAGGTTTTCATGACCTGCAGGATCTTCTTTCAGAGGCAT	1787
Qy	1900	TCACCTGAGGATAAAGAAGAAATATGATAAGACTTAAACAACATCTCCTCATCTTGTTC	1954
Db	1788	TCCACGAGCAACGAGGAGGAATACAGGCTCGGGGCTCTCGTCGCTCGTCGTCATC	1842

RESULT 14

AAV46276.	
ID	AAV46276 standard; cDNA; 1597 BP.
XX	
XX	AAV46276;
XX	
DT	16-OCT-1998 (first entry)
XX	
DE	A. thaliana N-terminal truncated NIM-1 variant cDNA #1.
XX	
KW	NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW	pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW	vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
XX	
OS	Arabidopsis thaliana.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FH	1..1410
CDS	/*tag= a
FT	/product= NIM-1
FT	/note= "variant"
FT	
XX	
PN	WO9829537-A2.
XX	
PD	09-JUL-1998.
XX	
PF	23-DEC-1997; 97WO-EP07253.
XX	
PR	10-JAN-1997; 97US-0035024.
PR	27-DEC-1996; 96US-0034378.
XX	
PA	(NOVS) NOVARTIS AG.
XX	
PI	Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;
XX	
WPI	1998-388119/33.
DR	P-PSDB; W6447.
XX	
XX	Protection of immunomodulated plants against pathogens - comprises
PT	applying microbicide to provide increase in resistance
XX	
PS	Claim 14; Page 123-127; 164pp; English.
XX	

CC This sequence encodes a truncated variant NIM-1 protein from Arabidopsis
CC thaliana. This protein is used in a method resulting in the protection of
CC an immunomodulated plant having a first level of resistance and involves
CC treatment with at least 1 microbicide that confers a second level of
CC resistance, such that the plants have a third level of resistance greater
CC than the sum of the first two levels. The method can be applied to a wide
CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
CC against viruses, fungi, bacteria, insects and nematodes. The method
CC provides a high level of resistance and allows a reduction in the amount
CC of microbicide used. Since the process involves two different methods of
CC protection, it is unlikely that the pathogen will develop resistance to
CC the treatment.

XX
SQ Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;

Query Match 25.3%; Score 549.4; DB 19; Length 1597;
Best Local Similarity 63.9%; Pred. No. 1.8e-138;
Matches 870; Conservative 0; Mismatches 476; Indels 15; Gaps 2;

QY 600 GATGCTGAATGAGTGATTGGCTTATTGTATGATGTTAAAGTTAGGCTTACCTAAA 659
DB 4 GATTCGGTTGGACTGTTTGGCTTATGTTTACAGCAGACAGTGAGCCGCCCTAAA 63
QY 660 GATGCTGTTGTTGTGCAAGTACGCTCTCATGTTGGCTTGTAGCCAGCTGTGGCA 719
DB 64 GGAGTTTCTGAATGCCAGACAGAGAATTGCTGCCACGTGGCTTGGCGCGCGGTGGAT 123
QY 720 TTCCCTGGTTAGGTTTGTACACATCATTTACCTTCAGATCTCTGAATGGTTGACAA 779
DB 124 TTATGTTTGGAGGTTCTCTATTGCTTTTCACTTCAAGATCCCTGGAATTAATCTCTC 183
QY 780 TTTCAGACACCTACTGGATTTCTTCACAAAAGTCGACGACGATGTAAATGATGTT 839
DB 184 TATCAGAGCCATTATTGGACGTTTACACAAAGTTGTTATAGGACACATTTGGTTATA 243
QY 840 TTATCTGTTGCAACATTTGTTGTTAAAGCATCGGAGAGATTGCTTTCAAGCTGCATTAG 899
DB 244 CTCAGCTTGCTTAATATATGTTGTTAAAGCTTGTTATGAAGCTATTGGATAGATTAAGAG 303
QY 900 ATTATGTCAAGCTTAATGTTGATATCATACCCCTTGATAAGGCTTCGCTCATGACATT 959
DB 304 ATTATGTCAAGCTTAATGTTGATATGTTTGTGTTGAAAAGTCAATGCCGGAAGAGCTT 363
QY 960 GTAAACAAATTTACTGATTTCAGGAGCGGAACCTTGGTCTACAAGGCGCTGAAGCAACGGT 1019
DB 364 GTTAAGAGATAATTGATAGAGCTTAAGAGCTTGGTTGGAGGTACCTAAAGTAA ---- 418
QY 1020 TTTCCTGATAACATGTTTAAGAGGATACATAGGCAATGGATTGATGATGTTGAATTA 1079
DB 419 -----AGAAACATGCTCTCGAATGTACATAAGGCACCTTGACTCGATGATTTGAGTTA 471
QY 1080 CTACAAATCTTCTAAGAGGGGCATACTACCCTAGATGATGATGCTCTCCATTAT 1139
DB 472 GTCAAGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATGCTGCTCTTCATTTC 531
QY 1140 GCTGTAGCGTATTGGGATGCAAGACTACAGCAGAACTTCTAGATCTTGCACCTTGCTGAT 1199
DB 532 GCTGTTGTCATATTGCAATGTGAAGACCGCAACAGATCTTTTAAAACTTGATCTCCCGAT 591
QY 1200 ATTAATCATCAAAATTCAGGGGATACAGGCTGCTGATGTTGCAAGCCATGAGGAAAGAG 1259
DB 592 GTCAACCATAGGAATCCGAGGGGATATACGGTGTCTCATGTTGCTGCGATGCGGAAGAG 651
QY 1260 CCTAAAATTTAGTGTCCTTTTAAACCAAGGAGCTAGACCTTCTGATCTGACATCCGAT 1319
DB 652 CCACATTTGATCTACTCTATTGGAAGAAAGTGCAAGTGCATCAGAGCACTTTGGAA 711
QY 1320 GGAAGAAAAGCACTTCAAAATGCCAAGAGGCTCACTAGGCTTTGTGATTTTCAGTAAGTCT 1379
DB 712 GGTAGAACCGCACTCATGATGCAAAAACCAAGCACTATGCGCGTTGAAATGTAATATATC 771
QY 1380 CCGGAGGAAGGAAATCTGCTTCGATGATCGTTTATGATTCATTTGAGATTTCTGGAGCAAGCA 1439

DB 772 CCGGAGCAATGCAAGCATTTCTCTCAAAGGCCGCACTATGTGTAGAAATACTAGACAAGNA 831
QY 1440 GAAAGAGAGACCCCTCTGCTAGGAGAGCTTCTGTATCTCTTCTGCTATGGCAGCGCATGAT 1499
DB 832 GACAAACGAGACAATTCCTAGAGATGTTCTCCCTCTCTTTGCACTGCGCGCATGAA 891
QY 1500 TTCCGATGAGCTGTTATACCTTGAATAGATGAGTTGGCTGGCTGCTTAACTCTCTTTTCCA 1559
DB 892 TTCAAGATGACGCTGCTCGATCTTGAATAAGATTTGCACTTGTCTCAAGCTCTTTTCCA 951
QY 1560 ATGGAAGCTAAAGTTGCAATGGACATTTGCTCAGTTGATGGCACTTCTCAGTTCCCACTG 1619
DB 952 ACGGAAGCACAGCTCAATGGAGATCGCGGAAATGAAGGAACATGTGAGTTTCATAGTG 1011
QY 1620 GCTAGCATCG---GCAAAAAGATGGCTAATGCACAGAGGACACACAGTAGATTGTAACGAG 1676
DB 1012 ACTAGCTCGAGCTGACCGCTCTCACTGGTACGAGAGAACAATCACCGGTTGTAAAGATA 1071
QY 1677 GCTCCTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTGTA 1736
DB 1072 GCACCTTTTCAAGATCTTAGAAGAGCATCAAAAGTAGACTAAAAGCGCTTTCTAAAACCGTG 1131
QY 1737 GAACCTTGGAAAACGCTTCTTCCACGTTGTCAGAAAGTTCTAAATGAAGATCATGGATGT 1796
DB 1132 GAACCTGGGAAACGATTTCTCCCGCTGTTCCGCGAGTGTCTGACAGATTTATGAAGTGT 1191
QY 1797 GATGACTTGTCTGAGATGATTTACATGGGGAATGATACGCGAGAGAGCGTCAACTGAAG 1856
DB 1192 GAGGACTTGACTCACTGGCTTCGGGAGAGAGACGACACTGCTGAGAAACGACTTACAAAAG 1251
QY 1857 AAGCAAGGTACATGGAACCTTCAAGAAATTTCTGACTAAAGCATTTCACTGAGGATAAAGAA 1916
DB 1252 AAGCAAGGTACATGGAATACAAAGAGACACTAAAGAGCGCTTTAGTGAGGACAAATTTG 1311
QY 1917 GAATATGATAGACTACACACATCTCTCATCTTGTTCCTC 1957
DB 1312 GAATTAGAAATTTGTCCTCGACAGATTCGACTTCTCCAC 1352
RESULT 15
AAVA3662
ID AAV3662 standard; cDNA; 1597 BP.
XX AAV3662;
XX AC
XX XX
DT 29-SEP-1998 (first entry)
XX Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA.
DE Non-inducible immunity-1 gene; NIM1 protein; disease resistance; mutant;
KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;
KW constitutive immunity; agriculture; variant; ss.
XX Arabidopsis thaliana.
OS Synthetic.
XX Key
FH CDS Location/Qualifiers
FT 1..1410
FT /*tag= a
FT /product= "NIM1 protein variant 2"
FT /note= "N-terminal deletion compared to wild-type
XX NIM1 sequence"
XX WO9825082-A1.
XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-EP07012.
XX 20-JUN-1997; 97US-0880179.
PR 13-DEC-1996; 96US-0033177.
PR 27-DEC-1996; 96US-0034379.
PR 27-DEC-1996; 96US-0034382.

PR 10-JAN-1997; 97US-0034730.
 PR 10-JAN-1997; 97US-0035021.
 PR 10-JAN-1997; 97US-0035022.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 XX Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;
 PI Uknes SJ;
 XX
 DR WPT; 1998-348536/30.
 DR P-PSDB; AAW61984.
 XX
 PT Use of non-inducible immunity-1 gene - for transforming plants to
 PT produce transgenic plants having a broad spectrum disease resistance
 XX
 PS Claim 9; Pages 149-152; 205pp; English.
 XX
 CC This cDNA encodes an altered form of the Arabidopsis thaliana non-
 CC inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to
 CC AAV43665 represent variants of the NIM1 cDNA. The invention provides a
 CC chimeric gene comprising a promoter active in plants operatively linked
 CC to a DNA molecule that encodes an altered form of the NIM1 protein. Plant
 CC cells stably transformed with a recombinant vector comprising such a
 CC chimeric gene have a broad spectrum of disease resistance. The altered
 CC NIM1 proteins act as dominant-negative regulators of the systemic
 CC acquired resistance (SAR) signal transduction pathway. The altered
 CC plants transformed with an altered NIM1 gene exhibits constitutive SAR
 CC expression which is higher in the transformed plants than in a wild-type
 CC plant. The products can be used for producing plants with a broad
 CC spectrum disease resistance. Overexpression of NIM1 mimics the effects
 CC of inducer compounds that induce constitutive immunity (CIM) phenotype
 CC in plants. The inventions can be used with plants such as rice, wheat,
 CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,
 CC chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,
 CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,
 CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,
 CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry,
 CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,
 CC tomato, sorghum and sugarcane. The plants produced are resistant to
 CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such
 CC as aphids and lepidoptera and nematodes. The plants produced can be used
 CC in agriculture.
 XX
 SQ Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;

Query Match 25.3%; Score 549.4; DB 19; Length 1597;
 Best Local Similarity 63.9%; Pred. No 1.8e-138;
 Matches 870; Conservative 0; Mismatches 476; Indels 15; Gaps 2;

QY 600 GATGCTGTATGAGTGATTTGGCTTATTTGTATAGTGGTAAAGTTAGGCCCTTCCACCTAAA 659
 DB 4 GATTTCGGTGTGACTGTTTGGCTTATGTTTACAGCAGCAGAGTGAGACCGCGCCTAAA 63
 QY 660 GATGCTGTGTTGTGGACATGACTGCTCATGTTGGCTTGTAGGCCAGCTGTGGCA 719
 DB 64 GGAGTTTCTGAATGCGCAGCAGAGAAATGCTGCCACGTGGCTTCCGCGCGCGGTGAT 123
 QY 720 TTCCTGCTTCCAGGTTTGTACACATCATTTTACCTTTTCAGATCTCTGAATTTGGTTGACAG 779
 DB 124 TTCATGTGGAGGTTCTCTATTTGGCTTTCATCTTCAAGATCCCTGAAATTAATTAATCTC 183
 QY 780 TTTCAGAGACACCTTACTGATATTTCTTGACAAAACCTGCAGCAGCATGTAATCATGGTT 839
 DB 184 TATCAGAGGCACATTATTGGAGCTTTGTAGACAAAGTTGTTATAGAGGACATTTGGTTATA 243
 QY 840 TTATCTGTTGCAACATTTGTGGTAAAGCATGCGAGATGCTTTTCAAGCTGCATGAG 899
 DB 244 CTCAGCTTCTCATATATGTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAG 303
 QY 900 ATATTCTCAAGTCTAATGTTGATATCATAAACCTTGTATAAAGCCTTGCCTCATGACATT 959
 DB 304 ATATTCTCAAGTCTAATGTTGATATGTTAGTCTTTGAAAGAGTCATTGCGCGGAAGAGCTT 363

QY 960 GTAAACAAATTTACTGATTCACGAGCGGAACTTGGTCTTACAAGGGCCTGAAAGCAACGGT 1019
 DB 364 GTTAAAGAGATAATTGATAGAGCTTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAA----- 418
 QY 1020 TTTCTGTATAAATCATGTTAAGAGGATACATAGGAGTTCGATTCTGATGATCTTGAATTA 1079
 DB 419 -----AGAACATGCTCGAATGTACATAAGGCACTTGACTCGGATGATATGAGTTA 471
 QY 1080 CTACAAATGTTGCTAAGAGAGGGGCATACCTACCTAGATGATGATGATGATGATGATGAT 1139
 DB 472 GTCAAGTTGCTTTTGAACAGGATCACACCAATCTAGATGATGCTGCTCTTCTTCAATTC 531
 QY 1140 GCTGTACGCTATTCGATGCAAGACTACAGCAGAACTTCTAGATCTTGCATCTTGCATGAT 1199
 DB 532 GCTGTGTCATATGCAATGTGAAGACCGCAACAGATCTTTTAAACCTTGATCTTCCGAT 591
 QY 1200 ATTAATCATCAAAATTCAGGGGATACAGGTGCTGATGTTGACGCCATGAGGAAGAG 1259
 DB 592 GTCAACCATAGGAATCCGAGGGGATATAGCGTCTTCACTGTTGCTGCGATCGGAAGAG 651
 QY 1260 CCTAAATTTGATGTCCTTTTAAACAAAGGAGCTAGACCTTCTGATCTGACATCCGAT 1319
 DB 652 CCACAAATTGATCTATCTATTGGAAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAA 711
 QY 1320 GGAAGAAAAGCACTTCAAAATCCCAAGAGGCTCAGTAGGCTTGTGGATTTCAAGTCT 1379
 DB 712 GGTAGAACCGCACTCATGATCGCAAAACCAAGCACTATGCGCGTTGAATGTAATAATATC 771
 QY 1380 CCGGAGGAAGGAAAAATCTGCTTCGAATGATCGGTTGATGATGATGATGATGATGATGATGAT 1439
 DB 772 CCGGAGCAATGCAAGCAATCTCTCAAGGCCGCACTATGTTGTAAGAACTACTAGAGCAAGAA 831
 QY 1440 GAAAGNAGAGCCCTGCTGAGAGAGAGCTTCTGATCTTCTGCTGATGCGAGCGGATGAT 1499
 DB 832 GACAAACGAGAACTTCTAGAGATGTTCTCCCTCTTTTGCAGTGGCGGCGCATGAA 891
 QY 1500 TTGCGTATCAAGCTGTTATACCTTGAATAAGATGTTGGCTTGGCTTAACTCCCTTTTCCA 1559
 DB 892 TTGAAGATGACGCTGCTCGATCTTGAATAAGATGTTGCACTTGTCTCAAGCTCTTTTCCA 951
 QY 1560 ATGGAAGCTAAAGTTGCAATGACATTTGCTCAAGTTGATGGAAGCTTCTGAGTTCCCACTG 1619
 DB 952 ACGGAAGCACAAAGCTCAATGGAGATCGCGAAATGAAGGGAACATGTGAGTTTCATAGTG 1011
 QY 1620 GCTAGCATCG---GCAAAAAGATGCTTAATGCACAGAGACAAACAGTAGATTGAACGAG 1676
 DB 1012 ACTAGCTCGAGCCTGACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATA 1071
 QY 1677 GCTCCTTTTCAAGATAAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAGAACTGTA 1736
 DB 1072 GCACCTTTTCAAGATCCTAGAGAGCATCAAGTAGACTAAAAGCGCTTCTTAAACCGTG 1131
 QY 1737 GAACTTGGAAAACGCTTCTTTTCCAGCTTGTTCAGAAAGTTCTAAATAGATCATGATGATCT 1796
 DB 1132 GAACTCGGGAAAACGATCTTCCCGCGCTGTTCGGCAGTGTCTCGACCATGATTAAGACTGT 1191
 QY 1797 GATGACTTCTCTGAGATAGCTTTACATGGGATGATAGCGGAGAGACGCTCAACTGAAG 1856
 DB 1192 GAGGACTTTCAGCTCAACTGGCTTGGCGAAGAGACGACACTGCTGAGAAAACGACTACAAAAG 1251
 QY 1857 AAGCAAGGTACATGGAAGCTTCAAGAAATTTCTGACTTAAAGCATTCACCTGAGGATAAAGAA 1916
 DB 1252 AAGCAAGGTACATGGAATCAAGAGACACTTAAGAGAGGCTTGTAGTGAGGACAAATTG 1311
 QY 1917 GAATATGATAAGACTTAACAACATCTCTCATCTCTTCTTCTCCT 1957
 DB 1312 GAATTAGGAAATTTGTCCTGACAGATTCGACTTCTCTCCAC 1352

Search completed: October 7, 2002, 22:58:47
 Job time : 253.181 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 22:39:34 ; Search time 47.2395 Seconds
(without alignments)
11293.859 Million cell updates/sec

Title: US-08-908-884-13
Perfect score: 2172
Sequence: 1 GTGACATTCTACTATGGCT.....ATTGAAAAA.....2172

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	576.8	26.6	2011	2	US-08-989-478-6
2	576.8	26.6	2011	2	US-08-989-478-7
3	576.8	26.6	2011	3	US-08-996-685-6
4	576.8	26.6	2011	3	US-08-996-685-7
5	549.4	25.3	1597	2	US-08-989-478-9
6	549.4	25.3	1597	3	US-08-996-685-9
7	517.4	23.8	1608	2	US-08-989-478-11
8	517.4	23.8	1608	3	US-08-996-685-11
9	490	22.6	1194	2	US-08-989-478-13
10	490	22.6	1194	3	US-08-996-685-13
11	326.8	15.0	5655	2	US-08-989-478-1
12	326.8	15.0	5655	3	US-08-996-685-1
13	326.8	15.0	5655	3	US-08-880-179-2
14	326.8	15.0	9919	3	US-08-880-179-1
15	316.2	14.6	786	2	US-08-989-478-15
16	316.2	14.6	786	3	US-08-996-685-15
17	49.4	2.3	7218	1	US-08-232-463-14
18	45.2	2.1	7218	1	US-08-232-463-14
19	41.8	1.9	3095	6	5231168-1
20	40.8	1.9	5261	1	US-08-045-806-3
21	40.8	1.9	5261	1	US-08-366-051B-3
22	39	1.8	6152	4	US-08-973-462-1
23	38.2	1.8	11225	6	5182210-9
24	37.4	1.7	18073	4	US-09-078-294-12
25	37	1.7	691	4	US-08-630-915A-220
26	37	1.7	2859	2	US-08-506-340A-2
27	36.8	1.7	80595	4	US-09-078-294-3

Sequence 595, App
Sequence 389, App
Sequence 388, App
Sequence 4, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 13, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 4, Appli

28 36.4 1.7 658 4 US-08-998-416-595
29 36.2 1.7 613 4 US-09-328-111-389
30 36.2 1.7 667 4 US-09-328-111-388
31 35.8 1.6 161 4 US-08-952-061-4
32 35.8 1.6 394 2 US-08-623-906A-7
33 35.4 1.6 1364 1 US-08-265-087-3
34 35.4 1.6 1364 1 US-08-621-493-3
35 35.4 1.6 1364 2 US-08-965-688-3
36 35.4 1.6 1364 4 US-09-260-173-3
37 35.2 1.6 510 2 US-08-934-959-7
38 35.2 1.6 2274 3 US-08-492-459-13
39 35.2 1.6 2274 3 US-08-423-752-13
40 35.2 1.6 2274 4 US-08-716-873-27
41 35.2 1.6 2274 4 US-09-368-431-27
42 35.2 1.6 2274 4 US-09-414-006-13
43 35 1.6 1815 4 US-09-586-935-2
44 34.6 1.6 2489 3 US-09-141-047-7
45 34.2 1.6 80246 4 US-09-078-294-4

ALIGNMENTS

RESULT 1
US-08-989-478-6
; Sequence 6, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911

: TELECOMMUNICATION INFORMATION:

[illegible]

RESULT 2

```

US-08-989-478--7
; Sequence 7, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
;

```

NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 5986082artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NO. 5986082th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:

NAME/KEY: CDS
LOCATION: 43..1824
OTHER INFORMATION: /product= "altered form of NIM1"
OTHER INFORMATION: /note= "Serine residues at amino acid positions 55 and 59 in wild-type NIM1 gene product have been changed to Alanine residues."
OTHER INFORMATION: wild-type NIM1 gene product have been changed to Alanine residues."
OTHER INFORMATION: wild-type NIM1 gene product have been changed to Alanine residues."
OTHER INFORMATION: wild-type NIM1 gene product have been changed to Alanine residues."

NAME/KEY: misc.feature

LOCATION: 205..217

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

275 CTTTCCACCGGTCGGTTTGTCTCAGCGAGAGCTCTTTCTTCAAGACGCGCTTTAGCGCGG 334
QY 535 AAAAGGAGAAGATACTAGT-----AAGTGGAAATTGAAGGAGGTGA 576
Db 335 CTAAAGAGGAGAAGACTCCAACAACACCGCCCGCTGAAGCTCGAGCTTAAGGAGATTG 394
QY 577 TGAAGAGCATGAGGTGAGCTATGATGCTGTATGATGATGATGATGATGATGATGATG 536
Db 395 CCAAGGATTACGAAGTCGGTTTCGATTTCGGTTGTGACTGTTTGGCTTATGTTTACAGA 454
QY 637 GTAAAGTTAGGCTTCAACCTAAAGATGTGTGTTTGTGTGGACATGACTGCTCTCATG 696
Db 455 GCAGAGTGAGCGCGCCCTAAAGGATTTCTCAATGCCACACGAGAAATTCCTGCCAGG 514
QY 697 TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTC 756
Db 515 TGGCTTGTAGGCCAGCTGTGGCATTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTC 574
QY 757 AGATCTCTGAATTTGGTTGACAAGTTTTCAGAGACACCTACTGGATATTTCTTGACAAA 816
Db 575 AGATCTCTGAATTTGGTTGACAAGTTTTCAGAGACACCTACTGGATATTTCTTGACAAA 634
QY 817 CAGCAGCATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 876
Db 635 TTATAGAGGACACATTTGTTTATCTCAAGCTTGCCTAATATATGTTGTTAAAGCTTGTAT 694
QY 877 GATTGCTTCAAGCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 936
Db 695 AGCTATTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754
QY 937 ATAAAGCCTTGGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 996
Db 755 AAAAGTCATTGCCGGAAGAGCTTTTAAAGAGATATTTGATAGACGTAAGAGCTTGGTT 814
QY 997 TACAAGGCGCTGAAAGCAACGGTTTTTCTGTATAAATCTTAAAGAGGATACATAGGGAT 1056
Db 815 TGGAGGTACCTTAAGTAA-----AGAAACATCTCTCGAATGTACATAGGAC 862
QY 1057 TGGATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1116
Db 863 TTGACTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 922
QY 1117 ATGATCATATGCTCTCCATTATGCTGTAGCGTATTGCGATGATGATGATGATGATGATGAT 1176
Db 923 ATGATCGGTGCTCTCTCATTTTCGCTGTTGCTGATGATGATGATGATGATGATGATGATG 982
QY 1177 TTCTAGATCTTGACCTTGCTGATATTAATCATCAAAATTCAAAGGGATACACGGTCTGC 1236
Db 983 TTTTAAACTTGATCTTGGCGATGCAACCATAGGAATCCGAGGGGATATACGGTCTTC 1042
QY 1237 ATGTTGACCCATGAGGAAGAGCCTTAAATTTGATGTCCTTTTAAACCAAGGAGCTA 1296
Db 1043 ATGTTGCTCGATGCGGAAGAGGACACAAATGATGATGATGATGATGATGATGATGATG 1102
QY 1297 GACCTTCTCATCTGACATCCGATGGAAGAAAGAAAGCACTTCAATTCGCAAGAGGCTCACTA 1356
Db 1103 GTGCATCAAGCAACTTTTGGAGGTAGAACCCGACTCATGATGATGATGATGATGATGATGAT 1162
QY 1357 GGCCTTGTGATTTCAAGTCTCCGAGGAAGAAATTCCTTTCGAATGATCGGTTAT 1416
Db 1163 TGGCGGTTGAATGATTAATATATCCCGAGCAATGCAAGCATTTCTCTCAAGGCCGACTAT 1222
QY 1417 GCATGAGATTCTGAGCAAGCAGAAAGAGAGACCCCTCTGCTAGAGAGCTTCTGTAT 1476
Db 1223 GTGTAGAAATCTAGAGCAAGAAAGAAACAAACGAGAAACAAATTCCTAGAGATGTTCTCCCT 1282
QY 1477 CTCCTTGTATGCGAGCGGATGATTTGCGTATGAAGCTGTTTACCTTGAAATAGAGTTG 1536
Db 1283 CTTTTCGATGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342
QY 1537 GCGTGGCTAAATCTCTTTTCCAAATGGAAGCTTAAAGTTGCAATGACATTTGCTCAAGTTG 1596
Db 1343 CACTTGTCTCAAGCTCTTTTTCACGGAAGCACAAGCTGCAATGGAGATCGCGGAATGA 1402

Qy 817 CAGCAGCAGTCTAATGATGCTTTTATCTGTGCAACATTTTGGTAAAGCATCGGAGA 876
Db 635 TTATAGAGGACACATTTGGTTTACTCAAGCTGTCTAATATATGTGTAAGCTTGATACA 694
Qy 877 GATTGCTTTCAAGCTGCTATGAGATTTATGTCAGTCTAATGTTGATATCAATCCCTTG 936
Db 695 AGCTATTGGATAGATGTAAGAGATTTATGTCAGTCTAATGTTGATATGTTAGTCTTG 754
Qy 937 ATAAAGCCTTGCCTCATGACATTTGTAACAAATTTACTGATTCACGAGCGGAACCTTGTC 996
Db 755 AAAAGTCTATCCGGAAGAGCTTGTAAAGAGATAATTGATAGAGCTAAAGAGCTTGCTT 814
Qy 997 TACAAGGCCCTGAAGCAACGGTTTCTGATAACATGTTAAAGAGGATACATAGGGCAT 1056
Db 815 TGGAGTACCTAAAGTAA-----AGAAACATGTCCTCAATGTATACATTAAGGCAC 862
Qy 1057 TGGATTCGTGATGTTGAATTTACTACAAATGTTGCTAAGAGAGGGGATACCTACCTAG 1116
Db 863 TTGACTCGATGATTTGAGTTAGTCAAGTTGCTTTTGAAGAGGATCACACCATCTAG 922
Qy 1117 ATGATGCATATGCTCTCATATGCTGTAGCGTATTTGGATGCAAGAGCTACAGCAGAAC 1176
Db 923 ATGATGCTGTGCTCTCTCATTTGCTGTGCTATTTGCAATGTTGAAGACCGCAACAGATC 982
Qy 1177 TTCTAGATCTTGCACCTTCTGATATTAATCATCAAAATTCAGGGGATACAGGTGCTGC 1236
Db 983 TTTTAAACTTTGATCTTCCCATGTCACCATAGGAATCCGAGGGGATATACGGTGTCTC 1042
Qy 1237 ATGTTGACCCATGAGGAAGAGCCTTAAATTTAGTGTCTCCTTTTAAACCAAGAGAGCTA 1296
Db 1043 ATGTTGCTGCGATCGGAAGGAGCCACAAATGATATCTCTATTGGAANAAGTGCAA 1102
Qy 1297 GACCTTCTGATCTGACATCGCATGGAAGAAAGCACTTCAATGCCCAAGAGGCTCACTA 1356
Db 1103 GTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTCATGATCGCAAAACCAAGCACTA 1162
Qy 1357 GCTTGTGATTTTCAGTAAGTCTCGGAGGAAGAAATCTGCTCGAATCATCGGTTAT 1416
Db 1163 TGGCGGTTGATGTAATAATATCCGGAGCAATGCAAGCATCTCTCAAGGCCGACTAT 1222
Qy 1417 GCATTTGATCTTGGAGCAAGCAGAAAGAGAGACCCCTCTCTAGGAGAGCTTCTGTAT 1476
Db 1223 GTGTAGAAATCTAGAGCAAGCAAGCAAAAGCAAAATCTCTAGAGATGTTCTCCTCT 1282
Qy 1477 CTCTTGTCTATGCGAGCGCATTTTGGTATGAAGCTGTTTACTCTGAAATAGAGTTG 1536
Db 1283 CTTTGTGAGTGGCGGCGGATGAATTTGAAGATGACGCTGCTGATCTTGAAATAGAGTTG 1342
Qy 1537 GCCTGGCTAAACTCCTTTTCCAAATGGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTG 1596
Db 1343 CACTTGTCTCAAGCTCTTTTCCACGAGNAGCAAGCTGCAATGGAGATCCCGAATGA 1402
Qy 1597 ATGGCACTTCTGAGTCTCCACTGCTAGCATGCG--GCAAAAAGATGCTTAATGCACAGA 1653
Db 1403 AGGGAACATGTGAGTTTATAGTACTAGTACTGACCTCGACCTCTCATGTTGACGAAGA 1462
Qy 1654 GGACAACAGTAGATTTGAACAGGCTCTTTCAAGATAAAGAGGAGGACCTTGAATCGGC 1713
Db 1463 GAACATCACCGGGTGAAGATAGACCTTTCAAGAACTCTAGAGAGCATCAAAAGTAGAC 1522
Qy 1714 TTAGAGCACTCTCTAGAACTGTAGAACTTGGAACCGCTTTTCCAGCTGTTGTCAGAAG 1773
Db 1523 TAAAGCGCTTTCTAAACCGTGAACCTCGGAACGATTTCTCCGCGCTGTTCCGCGAG 1582
Qy 1774 TTCTAATAGATCATGATGCTGATGCTGTGCTGAGATAGCTTTACATGGGGAATGATA 1833
Db 1583 TGCTCGACCAAGATTTGAACCTGTAGGACTTGACTCAACTGGCTTGGCGAAGACGACA 1642
Qy 1834 CGCAGAGAGCGTCACTGAGAGCAAGAGGTACATGGAATCTCAAGAAATTTCTGACTA 1893
Db 1643 CTGCTGAGAACGACTCAAAAAGAGCAAGGATACATGGAAATACAAGAGACACTAAGA 1702

Qy 1894 AAGCATTCAGTCAAGATTAAGAGAAATATGATAAGACTAAACAACATCTCCTCATCTTGT 1953
Db 1703 AGGCTTTAGTGAGGACAAATTTGGAATTAAGAAATTTGTCCTGACAGATTCGACTTCTT 1762
Qy 1954 CQCT 1957
Db 1763 CCAC 1766

RESULT 4
US-08-996-685-7
; Sequence 7, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Rues, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/P1/GC1912
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION: FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1824
OTHER INFORMATION: /product= "altered form of NIM1"
/note= "Serine residues at amino acid positions 55 and 59 in
wild-type NIM1 gene product have been changed to Alanine
residues."
OTHER INFORMATION: residues."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 205..217
OTHER INFORMATION: /note= "nucleotides 205 and 217
changed from T's to G's compared to wild-type sequence."
US-08-996-685-7

Query Match 26.6%; Score 576.8; DB 3; Length 2011;
Best Local Similarity 62.7%; Pred. No. 1.5e-155;
Matches 981; Conservative 0; Mismatches 547; Indels 36; Gaps 4;

QY 415 CGAGTTTGACTACTTCCGCGGAGCTAAAGCTTGTGGTTTCCGCGCCGCTGAAGGAAATTC 474
DB 218 CGCGGATGATTTCTACAGCGAGCTTAAAGCTTGTCTCCGAC---GGCCGGGAAATTT 274
QY 475 CGGTGACCGGTGCATTTTGTGGCGGAGGAGTCCGTTCTTTAAGAAATTTGTCTGCGGTA 534
DB 275 CTTTCCACCGGTGCTTGTACGAGAGCTCTTTCTTCAAGACGCTTTAGCCGCG 334
QY 535 AAAAGGAGAGAAATAGTAGT-----AAGTGGAAATTTGAAGGAGTGA 576
DB 335 CTAAGAGGAGAAAGAACTCCAAACACCGCGCGCTGAAGCTCGAGCTTAAGGAGATTG 394
QY 577 TGAAGAGCATGAGGTGAGCTATGATGCTGTAATGAGTATTTGGCTTATTTGTATAGTG 636
DB 395 CCAAGGATTAAGAAAGTCGGTTTCGATTCGGTTGTGATCTTTTGGCTTATTTTACAGCA 454
QY 637 GTAAAGTTAGGCTTCCACCTAAAGATGTGTGTTTGTGGACAACTACTGCTCTCATG 696
DB 455 GCAGGTGAGACCCGCGCTTAAGAGATTTCTGAATGCGCAGACGAGAAATGCTGCCAAG 514
QY 697 TGGCTTGTAGGCGAGCTGCGCAATTCCTGGTTGAGGTTTGTACACATCAATTTACCTTTC 756
DB 515 TGGCTTGGCGCGCGGGGTGATTTTCATGTTGGAGGTTCTCTATTTGGCTTTTCATCTTCA 574
QY 757 AGATCTGTAATTTGTTGACAACTTTTCAGACACCTACTGGATATTTCTTGACAAAACG 816
DB 575 AGATCCCTGAATTAATTAATCTCTATCAGAGGCATTTTGGACGTTGTAGACAAAGTTG 634
QY 817 CAGCAGACATGTAATGATGGTTTATCTCTGTGCAACAACTTTGTGTAAGCATGCGAGA 876
DB 635 TTATAGGACACATTTGGTTATCTCAAGCTTCTAATATATGTTGTAAGCTTTGTATCA 694
QY 877 GATTGCTTCAAGCTGATGAGATTTATGTTCAAGTCTTAATGTTGATATCAATACCTTTC 936
DB 695 AGCTATTTGGATGATTAAGAGATTTATTTCAAGTCTTAATGATGATATGTTTGTCTTTC 754
QY 937 ATAAAGCTTTCCTCTATGACATTTTAAACAAATTTACTGATTCACGCGGAACTTGGTC 996
DB 755 AAAAGTATTTCCGAGAGAGCTTTTAAAGAGATTAATTTGATGACCTAAAGAGCTTGGTT 814
QY 997 TACAAGGCGCTGAAAGCAACGGTTTCTCTGATAAATCATTTAAGAGGATACATAGGCGAT 1056
DB 815 TGGAGGTACCTAAAGTAA-----AGAAACATGCTCGAATGTACATAAGGCAC 862
QY 1057 TGGATTCTGATGATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1116

DB 863 TTGACTCGGATGATATTAGTGTAGTCAAGTTGCTTTTGAAGAGGATCAACCAATCTAG 922
QY 1117 ATGATGATATGCTCTCCATTTATCTGATCGTATTCGATGATCAAGAGCTACAGCAGAAC 1176
DB 923 ATGATGCTGTGCTCTTCATTTCCCTGTTGCATATTCGAATGTGAAGACCGCAGCATC 982
QY 1177 TCTAGATCTTTCACCTTGTGATATTATCATCAAAATTCGAAGGGATACAGGTGCTGC 1236
DB 983 TTTTAAACCTTGATCTTCCGATGTCACCATAGCAATCCGAGGGATATACGCTGCTTC 1042
QY 1237 ATGTTGAGCATCAGGAAGAGAGCTAAATTTAGTGTCCCTTTTAAACCAAGAGGACTA 1296
DB 1043 ATGTTGCTCGATCGGAAGAGGACCAATTTGATATCTCTATTGGAAGAGGTCGAA 1102
QY 1297 GACCTTCTGATCTGACATCCGATCGGAAGAAAGCACTTCAAAATCGCCAGAGGCTCACTA 1356
DB 1103 GTGATCAGAAGCAACTTTGGAAGTAGACCCGCACTCATGATCGCAAAACAGCCACTA 1162
QY 1357 GCGTTGTGATTTTCAGTAAGTCTCCGAGGAGGAAATTCGTTTCGAATGATCGGTTAT 1416
DB 1163 TGGCGTTTGAATGTAATAATATCCGGAGCAATGCAAGCAATTCCTCAAGGCGGACTAT 1222
QY 1417 GCATTGAGATTTCTGAGCAACGCAAGAGAGACCCCTCTCTAGGAGAGAGCTTCTCTAT 1476
DB 1223 GTGTAGAAATTAAGTGAAGAGCAAAACGAGAACTTTCTAGAGATGTTCTCCCT 1282
QY 1477 CTCCTGCTATGCGGCGGATGATTTGCGTATGAAGCTGTTATACCTTTGAAATAGAGTTG 1536
DB 1283 CTTTTCAGTGGCGCGGATGATTTGAAGATGAGCTGCTCGATCTTTGAAATAGAGTTG 1342
QY 1537 GCGTGGCTTAACTCCTTTTCCAAATGGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTG 1596
DB 1343 CACTTGCTCAACGCTTTTTCACGGAAGCAAGCTGCAATGGAGATGCGCCGAAATGA 1402
QY 1597 ATGCACTTCTGAGTTCCTGCTGCTAGCATCG---GCAAAAAGATGGCTAATGCACAGA 1653
DB 1403 AGGAAACATGTGAGTTTCATGATGACTAGCCTCGAGCCTGACCGCTCCTGCTGACGAGA 1462
QY 1654 GGACAACTAGTATGATTTGAACGAGGCTCTTTCAAGATATAAGAGAGGAGCACTTTGAATCGGC 1713
DB 1463 GAACATCACCGGGTGTAAAGATAGCACTTTTCAAGATCTTAGAAGAGCATCAAGATAGAC 1522
QY 1714 TTAGAGCACTCTTGAAGCTGTAGAACTTTGGAAGCTTCTTCCACGTTGTTTCCAGAG 1773
DB 1523 TAAAGAGCTTTTCAAAACCGTGAAGCTCGGGAACGATTTCTCCCGCTGTTTGGCAG 1582
QY 1774 TTTTAAATAGATCATGATGCTGATGATTTGCTGATAGATGCTTACATGGGAATGATA 1833
DB 1583 TGCTGCGACGATTAAGCTGTGAGGACTTGTACTCACTGCTTGGGAGAGACGACACA 1642
QY 1834 CGGCAAGAGCGTCACTGAAGAGCAAGGATACATGGAATTTCAAGAAATTTCTGACTA 1893
DB 1643 CTGCTGAGAAACGACTACAAAGAGCAAGGATACATGGAATACAAAGAGACACTAAAGA 1702
QY 1894 AAGCTTCACTGAGATTAAGAAATATGATAGACTAACAACATCTCTCATCTTTGTT 1953
DB 1703 AGGCTTTAGTGAGGACAAATTTGGAATTTAGGAAATTTTGTCCCTGACAGATTCGACTTCT 1762
QY 1954 CQTC 1957
DB 1763 CCAC 1766

RESULT 5
US-08-989-478-9
; Sequence 9, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

QY 1857 AACCAAGGTACATGCACTTCAAGAAATTCGACATAAGCACTTCACTGAGTAAGAA 1916
|||||
Db 1252 AAGCAAGGTACATGCACTTCAAGAAATTCGACATAAGCACTTCACTGAGTAAGAA 1311
|||||
QY 1917 GAATATGATGAAGTACATGCACTTCAAGAAATTCGACATAAGCACTTCACTGAGTAAGAA 1917
|||||
Db 1312 GAATAGGAATTTGTCCTGACAGATTCGACATTCCTCCAC 1352

RESULT 6

US-08-996-685-9

: Sequence 9, Application US/08996685

: Patent No. 6031153

: GENERAL INFORMATION:

: APPLICANT: Ryals, John

: APPLICANT: Friedrich, Leslie

: APPLICANT: Utnes, Scott

: APPLICANT: Molina, Antonio

: APPLICANT: Russ, Wilhelm

: APPLICANT: Knauf-Beiter, Gertrude

: APPLICANT: Kung, Ruth

: APPLICANT: Kessmann, Helmut

: APPLICANT: Oostendorp, Michael

: TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

: NUMBER OF SEQUENCES: 32

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: No. 6031153artis Corporation

: STREET: 3054 Cornwalis Road

: CITY: Research Triangle Park

: STATE: No. 6031153th Carolina

: COUNTRY: USA

: ZIP: 27709

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/996,685

: FILING DATE:

: CLASSIFICATION:

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/761,543

: FILING DATE: 6-DEC-1996

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/034,378

: FILING DATE: 27-DEC-1996

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/034,379

: FILING DATE: 27-DEC-1996

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/034,382

: FILING DATE: 27-DEC-1996

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/034,730

: FILING DATE: 10-JAN-1997

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/035,021

: FILING DATE: 10-JAN-1997

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/035,022

: FILING DATE: 10-JAN-1997

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/035,024

: FILING DATE: 10-JAN-1997

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/875,015

: FILING DATE: 16-JUL-1997

: ATTORNEY/AGENT INFORMATION:

: NAME: Meigs, J. Timothy

: REGISTRATION NUMBER: 38,241

: REFERENCE/DOCKET NUMBER: PF/S-21215/P1/CGC1912

: TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
OTHER INFORMATION: /product= "Altered form of NIM1"
OTHER INFORMATION: /note= "N-terminal deletion compared to wild-type NIM1"
OTHER INFORMATION: sequence."
US-08-996-685-9

Query Match 25.3%; Score 549.4; DB 3; Length 1597;

Best Local Similarity 63.9%; Pred. No. 9.6e-148;

Matches 870; Conservative 0; Mismatches 476; Indels 15; Gaps 2;

QY 600 GATGCTGTAAGTACGATGTTGGCTTATTTGTATAGTGTAAAGTTAGGCTTCACTTAA 659

Db 4 GATTCGGTTGTGACTGTTTGGCTTATTTGTATAGTGTAAAGTTAGGCTTCACTTAA 63

QY 660 GATGCTGTAAGTACGATGTTGGCTTATTTGTATAGTGTAAAGTTAGGCTTCACTTAA 719

Db 64 GGAGTTTCTGAATGCGCAGACGAGAAATTTGCTGCCACGTTGGCTTCCCGCGCGTGGAT 123

QY 720 TTCTGTTGTTGAGTTTGTACATCATTTACCTTTACAGATCTCTGAATTTGGTTGACAG 779

Db 124 TTCAATGTTGGAGTTCTCTATTTGGCTTTTCATTTCAAGATCCCTGAATTAATTAATCTC 183

QY 780 TTTCAGACACCTACTGATATTTCTTACAAAGTCTGACAGACGATGTAATGATGTT 839

Db 184 TATCAGAGGCACTTATTTGACGTTGTAGCAAAAGTTGTTATAGGACACATTTGGTTATA 243

QY 840 TTATCTGTTGCAACATTTGTTGTAAGCATCCGAGAGATTTGCTTTCAAGCTGCATTTGAG 899

Db 244 CTCAGCTTGTATATATGTTGTAAGCTTGTATAGGCTTATTTGGATAGATGTAAGAG 303

QY 900 ATTATGTCAGTCAATGTTGATATATACCTTTGATAAGCTTTCCTTCATGACAT 959

Db 304 ATTATGTCAGTCAATGTTGATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 363

QY 960 GTAAACAAATTTACTGATTCACGAGCGGAATTTGCTTACAAAGGCTTCAAGGCTTCAAGCAACGGT 1019

Db 364 GTAAAGAGATTAATGATAGACGTTAAAGAGCTTGGTTGGAGGTACCTTAAAGTAA ---- 418

QY 1020 TTTCCTGATAAATGTTTAAAGAGATACATAGGCGATTTGGATTTCTGATGATGTTGAATTA 1079

Db 419 -----AGAAACATGTTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTA 471

QY 1080 CTACAAATGTTCTTAAGAGAGGCGATACCTCCCTAGATGATGATGATGATGATGATGATGATGAT 1139

Db 472 GTCAAGTTGCTTTTGAAGAGGATCACACCAATCTAGATGATGATGATGATGATGATGATGATGAT 531

QY 1140 GCTGTAGCGTATTTGGGATGCAAGAGACTACAGCAAGAACTTCTAGATCTTTCGACTTCTGCTGAT 1199

Db 532 GCTGTGATATTTGCAATGTAAGCCGCAACAGATCTTTTAAAGCTTGTATCTTCCCGAT 591

QY 1200 ATTAATCATCAAAATTCAGGGGATACAGGTTGCTGATGTTGAGCCATGAGGAAAGAG 1259

Db 592 GTCAACCATAGGAATCCGAGGGGATATAGGTTGCTTCTGATGTTGCTGCGATGCGGAAGAG 651

QY 1260 CCTAAATTTGATGTTCCCTTTTAAACCAAGGAGTGTAGACCTTCTGATCTGATCTGATCTGAT 1319

Db 652 CCACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711

QY 1320 GGAAGAAAGGCACTTCAAAATCCCAAGAGGCTTCACTAGGCTTGTGATTTCACTAGTCT 1379

Db 712 GGTAGAACCGCACTCATGATCGCAAAACCAAGCCACTATGGCGTTTGAATGTAATAATATC 771

QY	1380	CCGGAGGAAGGAAATCTGCTTGGAAATGATCGGTTATGCAATTGAGATTCTGGAGCAAGCA	1439
Db	772	CCGGAGCAATGCAAGCATTTCTCTCAAGGCCGACTATGTGTAGAAATACTAGAGCAAGAA	831
QY	1440	GAAAGAGAGACCCCTGCTAGGAGAGCTTCTGTATCTCTTTGCTATGGCAGCGCGATGAT	1499
Db	832	GACAAACGAGACAATACTCTAGAGATGTCTCCCTCTTTTGGAGTGGGGCGCGATGAA	891
QY	1500	TTCCGTATGAAGCTGTATACCTTCAAAATAGAGTTGGCTGGCTAAACTCTCTTTTCCCA	1559
Db	892	TTCAAGATGACGCTGCTCGATCTTGAAATAGAGTTGCATTGCTCAACGTCITTTTTCCA	951
QY	1560	ATGGAAGCTAAAGTTGCCAATGACATTCGTCAAGTTGATGGCACTCTGTAGTTCCCACTG	1619
Db	952	ACGGAAGACAAGCTGCAATGGAGATCCCGAAATGAAGGGAACATGTGAGTTTCATAGTG	1011
QY	1620	GCTAGCATCG--GCCAAAAGATGCTTAATGCACAGAGAGCAACAGTAGATTTCAACGAG	1676
Db	1012	ACTAGCCTCGAGCCTCACCGTCTCACTGGTAGAAGAAACATCACCGGTGTAAAGATA	1071
QY	1677	GCTCCTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACCTCTCTAGAACGTGA	1736
Db	1072	GCACCTTTTCAGAATCCTAGAAGAGCATCAAAAGTAGACTAAAGCGCTTCTAARACCGTG	1131
QY	1737	GAACTTGGAAAACGCTTCTTTCCAGCTGTTTCAGAAGTTCTAAATATAGATCATGGATGCT	1796
Db	1132	GAACTCGGAAAACGATCTTCTCCCGGCTTCTTCCGCACTGCTCGACACAGATTATGAACGT	1191
QY	1797	GATGACTTGTCTGAGATAGCTTACATGGGAATGATACGGCAGAGAGCGTCAACTGAAG	1856
Db	1192	GAGGACTTGACTCACTGGCTTTCGGGGAAGACGACATGCTGAGAACACACTACAAAG	1251
QY	1857	AAGCAAGGTACATGGAACCTTCAAGAAATTCGTACTAAAGCATTCACCTGAGGATAAAGAA	1916
Db	1252	AAGCAAGGTACATGGAATACAAGAGACACTAAGRAGGCCCTTACTGAGGACAATTG	1311
QY	1917	GAATATGAAGACTACAACATCTCCCTCATCTTGTTCCTC	1957
Db	1312	GAATTAGGAAATTTCCCTGACAGATTCGACTTCTTCCAC	1352

RESULT 7

```

US-08-989-478-11
; Sequence 11, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Kyals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:

```

```

RESULT 8
US-08-996-685-11
; Sequence 11, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Puess, Wilhelm
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43...1608
; OTHER INFORMATION: /product= "Altered form of NIM1"
; OTHER INFORMATION: /note= "C-terminal deletion compared to wild-type NIM1."
US-08-996-685-11
;
; Query Match 23.8%; Score 517.4; DB 3; Length 1608;
; Best Local Similarity 63.0%; Pred. No. 1.5e-138;
; Matches 882; Conservative 0; Mismatches 481; Indels 36; Gaps 4;

```

Qy	415	CGGAGTTTGACTACTCTCCGCGACGCTAAGCTCTGTGTTTCCGCGCCCGTGTAAAGGAAATTC	474
Db	218	CGCCGGATGATTTCTACGCGAGCGCTAAGCTTGTTCTCTCCGAC--GCGCGGGAAGTTT	274
Qy	475	CGGTGCACCGGTGCATTTTCTCGCGCAGGAGTCCGTTCTTTAAGAATTTGTTCTCGCGTA	534
Db	275	CTTTCCACCGGTGGTTTGTACGCGAAGACTCTTTCTTCAAGACGCTTTAGCCGCGT	334
Qy	535	AAAAGGAGAGAACTAGTAGT-----AAGTGGAAATGAAGGAGGTGA	576
Db	335	CTAAGAAGGAGAAAGACTCAACAACACCGCCGCGTGAAGCTCGAGCTTGAAGAGATTG	394
Qy	577	TGAAGAGCACTGAGGTGAGCTATGATGCTGTAATGAGTCTATTGGCTTATTGTATATAGT	636
Db	395	CCAAGGATTACGAGTCGGTTTCGATTCCGTTCTGACTCTTTGGCTTAIGTTTACACGA	454
Qy	637	GTAAGTTAGCCCTTACCTTAAAGATGTGTGTGTTGTGTGGACAATGACTGCTCTCATG	696
Db	455	GCAGAGTGAGACCGCCGCTTAAAGGAGTTTCTGAATCGCAGACGAGAATTGCTGCCACG	514
Qy	697	TGGCTTGTAGCCGAGCTGTGGCAATTCCTGGTTCAGTCTTTGTACACATCATTTACCTTTC	756
Db	515	TGGCTTCCGCGCCGCGGTGGATTTCATGTTGGAGGTTCTTATTTGGCTTTTCATCTTCA	574
Qy	757	AGATCTCTGAATTTGGTTGACAAGTTTTCAGAGACACCTACTGTGATATCTTGACAAAACGT	816
Db	575	AGATCCCTGAATTAATTACTCTCTATCAGAGGCACCTATTGGACCTTGAGACAAAGTTG	634
Qy	817	CAGCAGACGATGTAATGATGGTTTTATCTGTTTGCACAAATTTTGGTAAAGCATGCGAGA	876
Db	635	TTATAGAGGACACATTTGGTTATCTCAAGCTTTGCTAATATATGTGGTAAAGCTTGATGA	694
Qy	877	GATTTGCTTTCAAGCTGCATTGAGATTATTTGCTCAAGTCTAATCTGATCATCAACCCCTG	936
Db	695	AGCTATTGGATAGATGTAAGAGATTATTTGCTCAAGTCTAATGATAGTATGTTAGTCTTG	754
Qy	937	ATAAGCCCTTGCCCTCATGACATTGTAACAAATTAATGATTACGAGCGGAACTTGGCT	996
Db	755	AAAAAGTCAATTCGCGGAAGAGCTTTGTTAAAGAGATATTTGATAGACGTAAAGAGCTTG	814
Qy	997	TACAAGGCCCTGAAGCAACCGGTTTTCCGTGATAAACATGTTAAGAGGATACATAGGCAT	1056
Db	815	TGGAGGTACCTTAAGTAA-----AGAACATGCTCTCGAATGTACATAGGCAC	862
Qy	1057	TGGATTCTGATGATGTTGAATTAATACTACAATGTTGCTAAGAGGGGATACTACCCCTAG	1116
Db	863	TTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTGAAGAGGATCACACCAATCTAG	922
Qy	1117	ATGATGATATGCTCTCCATTATGCTGTAGCTATTGGATGTCAAAGACTACACAGAAC	1176
Db	923	ATGATGGCTGTGCTCTTCATTTTCGCTGTGTCATATTGCAATGTGAAGACCGCAACATC	982
Qy	1177	TTCTAGACTTTGCACTTGCTTGATTTAATCATCAAAATTCGAAGGGGATACACGTTGCTG	1236
Db	983	TTTTAAAACTTGATCTTGCCGATGTCAACCATAGGAATCCGAGGGGATATACGTTGCTTC	1042
Qy	1237	ATGTTGCAGCCATGAGAAAGACCTTAAATTTGATGTGCTCCTTTTAAACAAAGAGGCTA	1296
Db	1043	ATGTTGCTGCGATGCGGAAGAGCCACAATTGATACTATCTCTATTGGAATAAGGTCGAA	1102
Qy	1297	GACCTTCTGATCTGACATCCGATGGAAGAAAAAGCACTTCAATCGCCAAGAGGCTCACTA	1356
Db	1103	GTGCATCAGAAGCAACTTTTGAAGGTAGAACCGCACTCATGATCGCAAAACACCCACTA	1162
Qy	1357	GGCTTGTGGAATTCAGTAACTCCTCGGAGGAAGGAAATCTGCTTCGAATGATCGGTTAT	1416
Db	1163	TGCGCGTTGAATGTAATAATATCCGCGAGCAATGCAAGCATTTCTCTCAAAGCGCGACTAT	1222
Qy	1417	GCATTGAGATTTCTGGAGCAAGCAGAAAGAGACCCCTCTGCTAGGAGAACCTTCTGTAT	1476
Db	1223	GTGTACAATACTAGAGCAAGAGAACAAACGAGAACAAATTCCTAGAGATGTTCTCCTCCCT	1382

QY	1477	CTCTTGCTATGGCAGGGATGATTTCCGCTATGAAGCTGTATACCTTGAAATAGAGTTG	1533
Db	1283	CTTTTTCAGTGGCGGGCGATGATTTGAAGATGACGCTGCTCGATCTTGAAATAGAGTTG	1342
QY	1537	GCCTGGCTAAACTCCTTTTCCAATGGAAGCTTAAAGTTGCAATGGACATTCGCTCAAGTTG	1596
Db	1343	CACCTTGCTCAACGCTCTTTTCCAACGGAAGCACAAGCTGCAATGGAGATCGCCGAATGA	1402
QY	1597	ATGCGACTTCTGAGTTCCCACTGGCTPAGCATCG---GCAAAAAGATGGCTTAATGCACAGA	1653
Db	1403	AGGGAACATGTGAGTTTCATAGTCACTAGCTAGCTCGAGCCTGACCGCTCTCACTGGTACGAAGA	1462
QY	1654	GGACAACAGTAGATTTCAACGAGGCTCCTTCAAGATAAAGAGAGGACGACTTGAATCGGC	1713
Db	1463	GAACATCCCGGGTGAAGATAGTACACCTTTTCAGAACTCTAGAAGAGCATCAAAAGTAGAC	1522
QY	1714	TTAGAGCACCTCTCTAGAACTGTAGAAGCTTGGAAAAAGCGTCTTTTCCAGCTTGTTTCAGAAG	1773
Db	1523	TAAAGGCGCTTTCTAAACCGTGGAACTCGGGAACAGATCTCTCCGCGCTGTTTCGCAG	1582
QY	1774	TTCTAATAAGATCATGGA	1792
Db	1583	TGCTCGACCAGATTATGAA	1601
RESULT 9			
US-08-989-478-13			
; Sequence 13, Application US/08989478			
; Patent No. 5986082			
; GENERAL INFORMATION:			
; APPLICANT: Uknes, Scott			
; APPLICANT: Hunt, Michelle			
; APPLICANT: Steiner, Henry-York			
; APPLICANT: Ryals, John			
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING			
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS			
; NUMBER OF SEQUENCES: 32			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: No. 5986082artis Corporation			
; STREET: 3054 Cornwallis Road			
; CITY: Research Triangle Park			
; STATE: No. 5986082th Carolina			
; COUNTRY: USA			
; ZIP: 27709			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/989,478			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/033,177			
; FILING DATE: 13-DEC-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/034,379			
; FILING DATE: 27-DEC-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/034,382			
; FILING DATE: 27-DEC-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/034,730			
; FILING DATE: 10-JAN-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/035,021			
; FILING DATE: 10-JAN-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/035,022			
; FILING DATE: 10-JAN-1997			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Meigs, J. Timothy			


```

; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DCKET NUMBER: PF/5-21215/P1/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1194
; OTHER INFORMATION: /product= "Altered form of NIM1"
; OTHER INFORMATION: /note= "N-terminal/C-terminal chimera."
;
US-08-996-685-13

Query Match          22.6%; Score 490; DB 3; Length 1194;
Best Local Similarity 64.5%; Pred. No. 8.8e-131;
Matches 771; Conservative 0; Mismatches 410; Indels 15; Gaps

QY   600  GATGCTGTAAAGTACGATGGCTATTGGCTTATTTGTATACGTGAAGTTAGCCCTTCACCTAAA    659
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    4     GATTCGGTTGTGACTGTTTTTGCTTATGTGCTTTACAGCAGCAGATGAGACGCCGCCCTAAA    63

QY   660  GATGTGTGTGTTTGTGTGCACAATCACTGCTCTCATGTGGCTTGFAGCCAGAGCTGTGSCA    719
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    64   GGAGTTTCTGAATGCCAGACCAGAATTCTGCCACGTGGCTTGCCGCCGCCGGTGGAT    123

QY   720  TTCCTGGTTGAGGTTTTGTACACATCATTTACCTTTTCAGATCTCTGAATGGTTTGACAAG    779
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    124  TTCATGTTGGAGGTTCTCTTATTTGGCTTTTCATCTTCAAAGATCCCTGAATTAATACTCTC    183

QY   780  TTTCAGACACACTACTCGATATTTCTTCGAAAACTCGACAGACGATCTTAATGATCGTT    839
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    184  TATCAGAGCACCTTATGGACCTTGTAGACAAGTTGTTATAGAGGACACATGGTTTATA    243

QY   840  TTATCTGTTGCAAACTTTGTGTAAGCATGCGAGATTGCTTTTCAAGCTGCATTGAG    899
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    244   CTCAAGCTTGCCTAAATATATGTGTAAGCTTGTATGAAGCTATTGGATAGATGTAAGAG    303

QY   900  ATTATTGTCAAGCTCTAAGCTTTCATATCATACCCCTTGATAAAGCCTTGCCCTCATGACATT    959
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    304  ATTATTGTCAAGCTCTAAGCTTTCATATCATACCCCTTGATAAAGCTTGTGTTGAGGACACAT    363

QY   960  GTAAAAAAATTAAGCTTTCAGAGCGGAACCTTGCTCTTCAAGGCCCTGAAAGCAACGGT    1019
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    364  GTTAAAGAGATAATTGATAGAGCTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAA-----    418

QY   1020  TTTCTGTATAACATGTTAAGAGGATACATAGGGCAATTTGATGATGTTGAATTA    1079
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    419  -----AGAACATGCTCTCGAATGTACATAGGCATTTGACTCGGATGATATTGAGTTA    471

```


Db 4147 GATCTTGAATAAGAGCT 4164

RESULT 12

US-08-996-685-1

/ Sequence 1, Application US/08996685

/ Patent No. 6031153

/ GENERAL INFORMATION:

/ APPLICANT: Ryals, John

/ APPLICANT: Friedrich, Leslie

/ APPLICANT: Uknes, Scott

/ APPLICANT: Molina, Antonio

/ APPLICANT: Ruess, Wilhelm

/ APPLICANT: Knauf-Beiter, Gertrude

/ APPLICANT: Kung, Ruth

/ APPLICANT: Kessmann, Helmut

/ APPLICANT: Oostendorp, Michael

/ TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

/ NUMBER OF SEQUENCES: 32

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: No. 6031153artis Corporation

/ STREET: 3054 Cornwallis Road

/ CITY: Research Triangle Park

/ STATE: No. 6031153th Carolina

/ COUNTRY: USA

/ ZIP: 27709

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/996,685

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/761,543

/ FILING DATE: 6-DEC-1996

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/034,378

/ FILING DATE: 27-DEC-1996

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/034,379

/ FILING DATE: 27-DEC-1996

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/034,382

/ FILING DATE: 27-DEC-1996

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/034,730

/ FILING DATE: 10-JAN-1997

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/035,021

/ FILING DATE: 10-JAN-1997

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/035,022

/ FILING DATE: 10-JAN-1997

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/035,024

/ FILING DATE: 10-JAN-1997

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/875,015

/ FILING DATE: 16-JUL-1997

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Meigs, J. Timothy

/ REGISTRATION NUMBER: 38,241

/ REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912

/ TELEPHONE: (919) 541-8587

/ TELEFAX: (919) 541-8689

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 5655 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: DNA (genomic)

/ HYPOTHETICAL: NO

/ ANTI-SENSE: NO

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 2787..3347

/ OTHER INFORMATION: /product= "1st exon of NIM1"

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 3427..4162

/ OTHER INFORMATION: /product= "2nd exon of NIM1"

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 4271..4474

/ OTHER INFORMATION: /product= "3rd exon of NIM1"

/ NAME/KEY: exon

/ LOCATION: 4586..4866

/ OTHER INFORMATION: /product= "4th exon of NIM1"

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)

US-08-996-685-1

Query Match 15.0%; Score 326.8; DB 3; Length 5655;

Best Local Similarity 58.6%; Pred. No. 1.3e-83;

Matches 714; Conservative 0; Mismatches 392; Indels 112; Gaps 4;

Qy 415 CGGAGTTTGACTACTTCCCGACGCTAAGCTTGCTGCGGCCCGTGTAAAGAAATTC 474

Db 2962 CGCGGATGATTCTACAGCAGCGCTAAGCTTGCTCTCCGAC---GGCGGGAAGTTT 3018

Qy 475 CGGTGCACCGGTGCAATTTGTCGGCAGGAGTCGCTTTTAAAGAAATTTGTTCTGCGGTA 534

Db 3019 CTTTCCACCGGTGGTGTGTCAGCGAGAGCTCTTTTCAAGAGCGCTTTAGCCCGCG 3078

Qy 535 AAAAGGAGAAGATAGTAGT-----AAGGTGGAATTAAGAGAGTGA 576

Db 3079 CTAAGAAGGAGAAGAGACTCCAAACACACCGCGCGCTGAAGCTCGAGCTTAAGGAGATTG 3138

Qy 577 TGAAGAGCATGAGGTGAGCTATGCTGTAATGAGTGTATGCGCTATTGTTATAGTG 636

Db 3139 CCAAGGATTACGAAGTGGTTTCGATTGCTGCTGTTGCTGCTTTGCTTTACAGCA 3198

Qy 637 GTAAAGTTAGCCCTTACCTAAAGATGTGTGTTGTGTGGACAATGACTGCTCTCATG 696

Db 3199 GCAGAGTGAGACCGCGCTAAAGGAGTCTCTGAATCGCAGACGAGAATTGCTGCCACG 3258

Qy 697 TGGCTTTAGGCCACGCTGCGCATTCCTGGTTGAGGTTTGTACACATCAATTTACCTTTC 736

Db 3259 TGGCTTGGCGCGCGGTGATTCATGTTGGAGGTTCTCTATTTGGCTTTTCATCTCA 3318

Qy 757 AGATCTCTGAAT-----768

Db 3319 AGATCCCTGATTAATTACTCTCTATCAGGTAACACCACTGTCATTAGCTATGGTTA 3378

Qy 769 -----TGGTTGACAAGTTTCAGACACACTACTG 797

Db 3379 CACATTTCATGAATATGTTCTTACTTTGAGTACTTGTATTGTTTATTCAGAGCACTATTG 3438

Qy 798 GATATTTCTGACAAACTGCAGCAGCAGTATGATGTTTATCTGTTGTTGCAACATT 857

Db 3439 GACGTTGACAAAGTTGTTATAGGAGCACACATTTGTTTACTCAAGCTTGTGAATATA 3498

Qy 858 TGTGTTAAAGCATGCGAGAGATTCTTTCAAGTGCATTCAGATTTATGTCAGTCTAAT 917

Db 3499 TGTGTTAAAGCTTGTATGAAGCTATTGGATAGATGTAAGAGATTTATGTCAGTCTAAT 3558

Qy 918 GTTGATATCATACCCCTTGATAAGCCTTGCCTCATGACATTTGTAACAAATTAAGTATGAT 977

Db 3559 GTAGATATGTTAGTCTTTGAAAGTCAATTCGCGAAGAGCTTCTTAAAGAGATAATTGAT 3618


```
Db 3379 CACATTCATGAATATGTTCTTACTTGTAGTACTTCTGATTTATTTGATGAGCGCACTTATTG 3438
QY 798 GATATCTTGACAAACAGTCAGCAGACGATGTAATGATGGTTTATCTGTGTGCAAAACATT 857
Db 3439 GACGTTGTAGACAAGATGTTATAGGACACATTTGTTATCTCAAGCTTGTCTAATATA 3498
QY 858 TGTGTTAAAGCATCGAGAGATTCCTTTCAAGCTGCAATGAGATTATTTGCAAGCTCTAAT 917
Db 3499 TGTGTTAAAGCTTGATGAAGCTATTGGATAGATGTAAGAGATTATTTGCAAGCTCTAAT 3558
QY 918 GTTGATATCATACCCCTGTATAAGCCCTTGCCCTCATGACATTTGTAACCAAAATTAAGTAT 977
Db 3559 GTAGATATGTTAGTCTTTGAAAAGTCATTCGCGAAGAGCTTGTATAAGAGATAATGAT 3618
QY 978 TCACGAGCGGAACCTGCTCTACAGGCGCTCAAGACCAACGGTTTCTGTATAAAGATGTT 1037
Db 3619 ACAGCTAAAGAGCTTGGTTTGGAGGTACCTAAAGTAAAG-----AAACATGTC 3666
QY 1038 AAGAGGATACATAGGCGAATGGATTCCTGATGATGTTGAATTAATCTACAAATGTTGCTAAGA 1097
Db 3667 TCGAATGTACATAAGGCACATGCTCGGATGATATTCAGTTAGTCAAGTTGCTTTTGAAA 3726
QY 1098 GAGGGGATACCTACCTAGATGATGATATGCTCTCCATTAATGCTGAGCGTATTCGGAT 1157
Db 3727 GAGGATCACACCAATCTAGATGATGCTGCTGCTCTCATTTCTGCTGTCATATGCAAT 3786
QY 1158 GCAAGGACTACAGCAGAACTCTAGATCTTGCATCTGCTGCTGATATTAATCATCAAAATTC 1217
Db 3787 GTGAAGACCGACAGATCTTTTAAACTTGTATCTTGCAGATGCAACCATAGGAATCCG 3846
QY 1218 AGGGATACACGGTGTCTGATGTTGCGACCATGAGGAAGAGCCTAAATGTTAGTGTCC 1277
Db 3847 AGGGATATACGGTGTCTGATGTTGCGATGCGGAGGAGCCACAATGATCTATCT 3906
QY 1278 CTTTTACCAAAAGAGCTAGACCTTCTGATCTGACATPCGATCGAAGAAAGCACTTCAA 1337
Db 3907 CTATFTGAAAAGAGTGAAGTGCATCAGAACCACTTTTGAAGGTAGAAGCGCACTCATG 3966
QY 1338 ATCCCAAGAGGCTCACTAGGCTTGTGGATTTTCAGTAAGTCTCGGAGGAGAAATCT 1397
Db 3967 ATCGCAAAACAGCCACTATGCGGTTGAATGTAATATCCGGAGCAATGCAAGCAT 4026
QY 1398 GCTTCGAATGATCGGTTATGATTTCTGGAGCAAGCAAGAAAGACCCCTCTG 1457
Db 4027 TCTCTCAAAGGCGACTATGTTAGAAATACTAGACGAAGACAAACAGACAAAT 4086
QY 1458 CTAGGAGAACCTCTGTATCTCTGCTATGCGCAGGCGATGATTTGCGTATGAGCTGTGTA 1517
Db 4087 CCTAGAGATGTTCTCTCCCTCTTTTGCAGTGGCGGCGATGAATGAAGATGACGCTGCTC 4146
QY 1518 TACCTTGAAAATAGAGTT 1535
Db 4147 GATCTTGAAAATAGAGT 4164
```

RESULT 14

US-08-880-179-1/c

Sequence 1, Application US/08880179

Patent No. 6091004

GENERAL INFORMATION:

```
APPLICANT: Ryals, John
APPLICANT: Delaney, Terry
APPLICANT: Friedrich, Leslie
APPLICANT: Weymann, Kristianna
APPLICANT: Lakton, Kay
APPLICANT: Ellis, Daniel
APPLICANT: Uknes, Scott
APPLICANT: Jesse, Taco
APPLICANT: Vos, Pieter
```

TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE

TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIS

TITLE OF INVENTION: IN PLANTS

```
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6091004artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880.179
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1909
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9919 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-880-179-1
```

Query Match 15.0%; Score 326.8; DB 3; Length 9919;

Best Local Similarity 58.6%; Pred No. 1.8e-83;

Matches 714; Conservative 0; Mismatches 392; Indels 112; Gaps 4;

```
QY 415 CGGAGTTTGACTACTTCGCCGACGCTAAGCTTGTGGTTTCGGCCGCGGTGAAGGAAATTC 474
Db 3600 CGCCGGATGATTTCTACAGCGACGCTAAGCTTGTCTCTCCGAC---GGCCGGGAAGTTT 3544
QY 475 CGGTCACCGGTGCACTTTGTCGGCGAGGAGTCGCTTCTTTAAGAAATTTGTTTCGGGTA 534
Db 3543 CTTTCCACCGGTGCGTTTGTGACGGAAGCTCTTTCTCAAGAGCGCTTTAGCCGCG 3484
QY 535 AAAAGGAGAAATAGTAGT-----AAGGTGAATTTGAAGGAGTGA 576
Db 3483 CTAAAGAGGAGAAAGACCTCCAAACACACCGCGCGTGAAGCTGAGCTTAAGGAGATTG 3424
QY 577 TGAAGAGCATGAGGTGAGCTATGATGCTGAATGAGTGTATTTGGCTTATTTGATAGTG 636
Db 3423 CCAAGGATTAGCAAGTCGGTTTCGATTCGGTTGTGACTGTTTGGCTTATCTTTACAGCA 3364
QY 637 GTAAAGTTAGGCTTCACCTAAAGATGTCGTGTTTGTGTGGACAATGACATGCTCTCATG 696
Db 3363 GCAGAGTGAGACCGCGCTTAAAGAGGTTTCTGAATGCGCAGACGAGAATTTGCTGCCACG 3304
QY 697 TGGCTTGTAGCCAGCTGTGGCATTCTCCTGTTGAGTGTGTTTGTACACATCATTTACCTTTC 756
Db 3303 TGGCTTGTGCGCGCGCGGTGGATTTCATGTTGGAGGTTCTCTATTTGGCTTTCATCTTCA 3244
QY 757 AGATCTCTGAAT-----TGCTTGCACAGTTTCAGAGACACCTACTG 797
Db 3243 AGATCCCTGAATTAATTAATCTCTATCAGGTAAACACCATCTGCATTAAAGCTATGTTA 3184
QY 769 -----TGCTTGCACAGTTTCAGAGACACCTACTG 797
Db 3183 CACATTCATGAATATGTTCTTACTTACTTGTAGTACTTGTATTTGATTTTCAGAGCACTTATG 3124
QY 798 GATATCTTGCACAAACTGCAGCAGCATGATGATGTTTATCTGTTGCAACATT 857
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..786
OTHER INFORMATION: /product= "Altered form of NIM1"
OTHER INFORMATION: /note= "Ankyrin domains of NIM1."
US-08-989-478-15
Query Match 14.6%; Score 316.2; DB 2; Length 786;
Best Local Similarity 64.3%; Pred. No. 4.9e-81;
Matches 496; Conservative 0; Mismatches 263; Indels 12; Gaps 1;
QY 555 AAGGTGGAATTGAAGGAGGTGATGAAGAGCATGAGGTGAGCTATGCTCTAATGAGT 614
DB 28 AAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTTCGATTCGGATTGCGT 87
QY 615 GTATTGGCTTATTGTATAGTGTAAAGTTAGCCCTTACCTTAAAGAGATGTGTGTGT 674
DB 88 GTTTGGCTTATGTTTACAGCAGCAGAGTGACGCCCTTAAAGAGATTCTCAATGC 147
QY 675 GTGCACATGACTGCTCTCATGTGGCTTGTAGGCAGCTGTGGCATTTCTGTGAGGTT 734
DB 148 GCAGACGAGAATTGCTGCCACGTGGCTTCCCGCGCGGGGTTCATGTTGAGGTT 207
QY 735 TTGTACACATCATTTACCTTTTCAGATCTCTGAATTGGTTGACAAGTTTCAGAGACACCTA 794
DB 208 CTCTATTTCGCTTTTCATCTTCAAGATCCCTGAAATTAATCTCTATCAGAGGCCTTA 267
QY 795 CTGTGATATTCTTGACAAAACCTGCAGCAGACGATGTAATGATGTTTATCTGTTGCAAC 854
DB 268 TTGGAGCTTTGTAGACAAAGTTGTGTAGAGGACACATGTTTATCTCAAGCTTCTAAT 327
QY 855 ATTTGTGTAAGCATGCGAGAGATTGCTTTCAAGCTGCAATTCAGATTATTTGCTCAAGTCT 914
DB 328 ATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATTGTAAGAGATTATTGCTCAAGTCT 387

```
QY 915 AATCTTGATATATAACCCCTTGATAAAGCCTTGCTCATGACATTTGTAACAACTTACT 974
    |||| |||| | | |||| | | |||| | | |||| |||| | | ||||
Db 388 AATGTAGATATGTTAGTCTTTGAAGAGTCATTGCCGAGAGAGCTTGTAAAGAGATAATT 447
    |||| |||| | | |||| | | |||| | | |||| | | |||| | | ||||
QY 975 GATTCAGAGCGGAACCTTGCTCTACAGGCGCTGAAGCAACGGTTTCTCTGATAAACAT 1034
    |||| |||| | | |||| | | |||| | | |||| | | |||| | | ||||
Db 448 GATAGACGTAAGAGAGCTTGGTTTGGAGGTACCTAAAGTAA-----AGAAACAT 495
    || || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
QY 1035 GTTAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAATTTGCTA 1094
    || || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 496 GTCTCGAATCTACATAGGCACCTGACTCGGATGATATTGAGTTAGTCAAGTTGCTTTTG 555
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
QY 1095 AGAGAGGGCATACTACCCCTAGATGATGCATATGCTCTCCATTATGCTGTAGCGTATTGC 1154
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
Db 556 AAAGAGGATCACACCAATCTAGATGATGGCTGCTCTTCATTTCCCTGTTGCATATTGC 615
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
QY 1155 GATGCAAGACTACAGCAGAACCTTCTAGATCTTGGCACTTGGTGANATTAATCATCAAAAT 1214
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
Db 616 AATGTGAAGACCGCAACAGATCTTTAAACTTTGATCTTCCGATGTCAACCATAGGAAT 675
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
QY 1215 TCAAGGGGATACACGGTGTGCTGTCATGTTGGAGCCATGAGGAAGAGCCTAAATTTAGTGTG 1274
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
Db 676 CCGAGGGGATATACGGTGTCTCAITGTTGCTGCGATGCGGAGAGGCCACAATTGATACTA 735
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
QY 1275 TCCCTTTTAAACCAAGAGCTAGACCTTCTGTATCTGACATCCGATGGAAGA 1325
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
Db 736 TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAGCAACTTTGGAGGTTGA 786
    |||| |||| | | |||| |||| |||| |||| |||| |||| |||| ||||
```

Search completed: October 8, 2002, 01:24:23
Job time : 116.239 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2002, 21:32:09 ; Search time 1696.05 Seconds
(without alignments)
17284.510 Million cell updates/sec

Title: US-08-908-884-13

Perfect score: 2172

Sequence: 1 GTGACTTCTCACTATGGCT.....ATTGAAAAAAAAAAAAAAAAA 2172

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	517.2	23.8	613	9	AW160235
2	457	21.0	654	10	BG124935
3	400.6	18.4	736	10	BE435499
4	354.2	16.3	516	9	AW622846
5	348	16.0	503	10	BE432768
6	316.2	14.6	614	10	BG464249
7	261.2	12.0	539	10	BI210424
8	249	11.5	557	9	AW160234
9	234.2	10.8	573	9	AV551266
10	232	10.7	455	10	BE493178
11	211.2	9.7	772	12	BH525927
12	198.2	9.1	700	10	BM111027
13	191.8	8.8	667	10	BG598808
14	179.6	8.3	458	9	BE023215
15	171.8	7.9	450	9	AW399343
16	167.2	7.7	547	10	BE918569
17	164	7.6	569	9	AW745943

c	18	163.6	7.5	463	12	BH211724
	19	162	7.5	491	10	BF657743
	20	161.6	7.4	576	10	BF096790
	21	157	7.2	588	10	BM307942
	22	152.6	7.0	805	10	BG414779
	23	150.2	6.9	744	10	BG526766
c	24	146.6	6.7	629	12	B26306
c	25	146.4	6.7	730	10	BI968818
	26	146	6.7	430	9	AI442277
	27	146	6.7	465	9	AW216501
	28	137.4	6.3	765	10	BG526883
	29	131.2	6.0	637	10	BG521476
	30	130.4	6.0	462	9	AL372473
	31	128.4	5.9	595	10	BE801977
c	32	128.4	5.9	645	9	AW310982
c	33	124.4	5.7	569	10	BE366197
c	34	123.6	5.7	781	12	BH483537
	35	122.8	5.7	562	10	BE366196
	36	118.6	5.5	577	10	BM324012
	37	115.8	5.3	535	9	AW687759
	38	114.6	5.3	593	9	AW618318
c	39	114.4	5.3	495	9	AI997958
c	40	112	5.2	680	9	AW309867
	41	110.8	5.1	461	9	AI960862
	42	108.6	5.0	258	10	T22612
	43	105.6	4.9	394	9	BE020423
c	44	105.2	4.8	733	9	AW349633
45	103.6	4.8	669	9	AW684122	

ALIGNMENTS

RESULT 1
AW160235/c
LOCUS
DEFINITION
EST290093 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT19 similar to A. thaliana transcription factor inhibitor I kappa B homolog, mRNA sequence.
ACCESSION
AW160235
VERSION
AW160235.1
KEYWORDS
EST.
SOURCE
Lycopersicon pennellii.
ORGANISM
Lycopersicon pennellii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
1 (bases 1 to 613)
AUTHORS
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E., Liang,F., Hansen,I.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii) trichomes
JOURNAL
Unpublished (1999)
COMMENT
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
3 prime sequence.
FEATURES
source
location/Qualifiers
1..613
/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT19"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid

nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."

BASE COUNT 159 a 148 c 107 g 199 t

ORIGIN

Query Match 23.8%; Score 517.2; DB 9; Length 613;

Best Local Similarity 93.1%; Pred. No. 9.1e-104;

Matches 564; Conservative 0; Mismatches 38; Indels 4; Gaps 2;

Qy 1430 GGAGCAAGCAAGAAAGAGACCCCTGCTAGGAGAGCTTCTGTATCTCTGCTATGCG 1489

Db 613 GGAGCAAGCAAGAAAGAGATCCACTACTAGGAGAGCTTCATTATCTCTGCTATGCG 554

Qy 1490 AGGGGATGTTGGGTATGAAGCTGTTATACCTTGAATAAGAGTTGGCTGGCTGAAC 1549

Db 553 AGGGGATGTTGGGTATGAAGCTGTTATACCTTGAATAAGAGTTGGCTGGCTGAAC 494

Qy 1550 CCTTTTCCCAATGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTGATGGCACTTCTGA 1609

Db 493 CCTTTTCCCAATGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTGATGGCACTTCTGA 434

Qy 1610 GTTCCCACTGCTAGCATGCGCAAAAAGATGGCTTAATGCGAGAGCAACAGTAGATTT 1669

Db 433 ATTACCCTGCTAGCATGAGGAGAAAGATAGCTGATGCGAGAGCAACAGTGGATTT 374

Qy 1670 GAACGAGCTCCTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAG 1729

Db 373 GAACGAGCTCCTTTCAAGATAAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTCTAG 314

Qy 1730 AACTGTAGAACTTGGAAACGCTTCTTCCACGTTGTTCCAGAACTTCTTAATAAGATCAT 1789

Db 313 AACTGTAGAACTTGGAAACGCTTCTTCCACGTTGTTCCAGAACTTCTTAATAAGATCAT 254

Qy 1790 GGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATCGGAGAGAGCGTCA 1849

Db 253 GGATGCTGATGACTTGTCTGAGATAGCTTACATGGGGAATGATCGAGTAGAAGAGCGTCA 194

Qy 1850 ACTGAAGAGCAAGGTACATGGAACCTTCAAGAAATCTGACTAAGCACTTCACTGAGGA 1909

Db 193 ACTGAAGAGCAAGGTACATGGAACCTTCAAGAAATCTGACTAAGCACTTCACTGAGGA 134

Qy 1910 TAAAGAAATATGATAGACTTAACAACATCTCCTCATCTTGTTCCTCTACATCTAAGGG 1969

Db 133 TAAAGAAATATGATAGACTTAAAGACTTAAAGACTTAAAGACTTAAAGACTTAAAGGG 77

Qy 1970 AGTAGATAGCCCAATAGCTCCCTTTTAGGAATAGGTAATTTGATATAGGATATAGAG 2029

Db 76 AGTAGATAGCCCAATAGCTCCCTTTTAGGAATAGGTAATTTGATATAGGATATAGAG 18

Qy 2030 GAAGAA 2035

Db 17 GAAGAA 12

RESULT 2

LOCUS BG124935

DEFINITION EST470581 tomato shoot/meristem Lycopersicon esculentum cDNA clone

ctof7k1 5' sequence, mRNA sequence.

ACCESSION BG124935

VERSION BG124935.1 GI:12625123

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.

1 (bases 1 to 654)

van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,

Hansen,C., Ronning,C. and Tanksley,S.

Generation of ESTs from tomato shoot/meristem tissue

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

Location/Qualifiers

1..654

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="ctof7k1"

/clone_lib="tomato shoot/meristem"

/tissue_type="shoot/meristem"

/dev_stage="developing shoots from 4-6wks old plants"

/lab_host="SOLR"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; Small expanding leaves from the growing tip were

taken from greenhouse plants (4-6wks old TA496). Tissue

was immediately frozen in liquid nitrogen."

BASE COUNT 218 a 110 c 145 g 181 t

ORIGIN

Query Match 21.0%; Score 457; DB 10; Length 654;

Best Local Similarity 88.0%; Pred. No. 1.8e-90;

Matches 552; Conservative 0; Mismatches 50; Indels 25; Gaps 4;

Qy 1497 GATTTGCGTATGAAGCTGTATACCTTGAATAATAGAGTTGGCTGCTAAACTCCCTTTT 1556

Db 2 GATTTGCGTATGAAGCTGTATACCTTGAATAATAGAGTTGGCTGCTAAACTCCCTTTT 61

Qy 1557 CCAATGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTGATGGCACTTCTGAGTCCCA 1616

Db 62 CCAATGAAGCTAAAGTTGCAATGGACATTTGCTCAAGTTGATGGCACTTCTGAGTCCCA 121

Qy 1617 CTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGCAACAGTAGATTTGAACGAG 1676

Db 122 CTGGCTAGCATCGGCAAAAAGATGGCTAATGCACAGAGCAACAGTAGATTTGAACGAG 181

Qy 1677 GCTCCTTCAAGATAAAGAGGAGGACACTTGAATCGGCTTAGAGCACTCTAGAACTGTA 1736

Db 182 GCTCCTTCAAGATAAAGAGGAGGACACTTGAATCGGCTTAGAGCACTCTAGAACTGTA 241

Qy 1737 GAACTTGGAAAACGCTTCTTCCACGTTGTTCCAGAGTTCTAAATAGATCATGGATGCT 1796

Db 242 GAACTTGGAAAACGCTTCTTCCACGTTGTTCCAGAGTTCTAAATAGATCATGGATGCT 301

Qy 1797 GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGCGAGAGCGTCAACTGAAG 1856

Db 302 GATGACTTGTCTGAGATAGCTTACATGGGGAATGATACGCGAGAGCGTCAACTGAAG 361

Qy 1857 AAGCAAGGTACATGGAACCTTCAAGAAATTTCTGACTAAAGCACTTCACTGAGGATAAGAA 1916

Db 362 AAGCAAGGTACATGGAACCTTCAAGAAATTTCTGACTAAAGCACTTCACTGAGGATAAGAA 421

Qy 1917 GAATATGATAAGACTAACACATCTCCTCACTTGTTCCTCTACATCTTAAGGAGTAGAT 1976

Db 422 GAATATGATAAGACTAACACATCTCCTCACTTGTTCCTCTACATCTTAAGGAGTAGAT 478

Qy 1977 AAGCCCAATAAGCTCCCTTTTAGGAAATAGGTAATGTTATTAGGATATATAGGAGGAAG 2036

Db 479 AAGCCCAATAAGCTCCCTTTTAGGAAATAGGTAATGTTATTAGGATATATAGGAGGAAG - 536

Qy 2037 AGGATTTTCTTGTAAACATAGCACTTCTCCTTTCATCATTTGATATGTCAACATACATAC 2096

Db 537 AGGATTTTCTTGTAAACATAGCACTTCTCCTTTCATCATTTGATATGTCAACATACATAC 576

Qy 2097 AACAGCTGTACCAATAAAGCTTGTATTGT 2123

Db 577 AACACATGTACCAATAAAGCTTGTATTGT 603

RESULT 3

```
BE435499      BE435499      736 bp      mRNA      linear      EST 18-MAY-2001
LOCUS      EST406577 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
DEFINITION      clone cLEG27M10, mRNA sequence.
ACCESSION      BE435499
VERSION      BE435499.1 GI:9433342
SOURCE      tomato.
ORGANISM      Lycopersicon esculentum
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
              Lycopersicon.
REFERENCE      1 (bases 1 to 736)
AUTHORS      Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
              Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
              Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
              ,S.D.
              Generation of ESTs from tomato fruit tissue, breaker stage
              Unpublished (2000)
              Contact: CUGI
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Email: http://www.genome.clemson.edu/orders/index.html
              5 prime sequence.
FEATURES      source
              Location/Qualifiers
                1..736
                  /organism="Lycopersicon esculentum"
                  /cultivar="TA496"
                  /db_xref="taxon:4081"
                  /clone_lib="cLEG27M10"
                  /clone_lib="tomato breaker fruit, TIGR"
                  /tissue_type="pericarp"
                  /dev_stage="breaker"
                  /lab_host="SOLR"
                  /note="Vector: pBluescriptSKmCuadapt; Site_1: EcoRI;
                  Site_2: XhoI; Fruit were harvested at the breaker stage
                  (first sign of lycopene accumulation on the blossom end of
                  the fruit). Fruit were cut in half and the seeds and
                  locules were discarded prior to freezing the pericarp."
BASE COUNT      185 a 152 c 166 g 233 t
ORIGIN
Query Match      18.4%; Score 400.6; DB 10; Length 736;
Best Local Similarity      80.7%; Pred. No. 4.9e-78;
Matches 517; Conservative      0; Mismatches 94; Indels 30; Gaps 3;

QY 247 ATAGTAGACTGGTTTCTCGATCGAATGACATCAGCGGAACAGTAGTATATGCTGCA 306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 ATAGTAGAAGTGGCTTTTCGGATTCCCAATGATATAGTGAAGCAGTAGTATGCTGCA 178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 307 TCGCGCGGCATGACTGAAATTTTCTCGCGCGAGACTTCGCGCGGAGACACTTTCAC 366
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 TGAACGAT-----CGGAAACTTTCAGTGGCAGACGTCATATCCC 217
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 TGAACGCCATCGGAACACTGGAATCTATCTTCGATCGCTTTTCGCGAGTTTGACT 426
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 TCAACGCTCTACAGAAACACTAGAGTCATCTTCGATCGCTGCGCGGATTCGACT 277
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 427 ACTTCGCGGACGTAGCTTGCTTTCGCGCGCGGTGAAGAAATTCGGTGCACCGGT 486
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 TCTTCGCTGATGCTAGCTTCTGGCTCCAGC---GGAAGGAAATTCGGTGCATCGGT 334
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 487 GCATTTTGTCCGGAGAGGAGTCGCTTCTTAAGAAATTTGTTCTCGCTAAAGGAGAA 546
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 335 GCATTTTGTCCGGAGAGGAGTCCTTTTAAAGAAATGATCTCTGTGGGAAA-----GATA 388
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 547 ATAGTAGAGTGAAGTGAAGGAGGTGATGAAGACGATGAGTGAGCTATGATGCTG 606
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 389 GCAACGAGAGTGGAACTCAAGAGCTGATGAAAGATGATGAGGTGAGTTTGTATGCCG 448
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 607 TAATGAGTGATGGCTTATTTGTATAGTGGTAAAGTTAGGCCTTCAACCTAAAGATGCT 666
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
AW622846/c      AW622846      516 bp      mRNA      linear      EST 18-MAY-2001
LOCUS      EST306916 tomato flower buds 3-8 mm, Cornell University
DEFINITION      Lycopersicon esculentum cDNA clone cTOB5H2 5', mRNA sequence.
ACCESSION      AW622846
VERSION      AW622846.1 GI:7335873
KEYWORDS      EST.
SOURCE      tomato.
ORGANISM      Lycopersicon esculentum
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
              Lycopersicon.
REFERENCE      1 (bases 1 to 516)
AUTHORS      van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang
              ,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W.,
              Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
              Generation of ESTs from tomato flower tissue, 3-8 mm buds
              Unpublished (1999)
              Contact: CUGI
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Email: http://www.genome.clemson.edu/orders/index.html
              5 prime sequence.
FEATURES      source
              Location/Qualifiers
                1..516
                  /organism="Lycopersicon esculentum"
                  /cultivar="TA496"
                  /db_xref="taxon:4081"
                  /clone_lib="cTOB5H2"
                  /clone_lib="tomato flower buds 3-8 mm, Cornell University"
                  /tissue_type="flower"
                  /dev_stage="3-8mm buds"
                  /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                  XhoI; supplier: Tanksley; Flower buds and flowers were
                  taken from greenhouse plants (4-8 wks old, TA496). They
                  were immediately frozen in liquid nitrogen and then
                  size-separated while remaining frozen."
BASE COUNT      142 a 110 c 87 g 177 t
ORIGIN
Query Match      16.3%; Score 354.2; DB 9; Length 516;
Best Local Similarity      92.5%; Pred. No. 8.6e-68;
Matches 395; Conservative      0; Mismatches 28; Indels 4; Gaps 2;

QY 1609 AGTTCCTCCACTGGCTAGCAGCGCAAAAAGATGGCTTAATGCAGAGGACACACAGTATT 1668
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 516 AATTACCCTCGCTAGCATGAGGAAGAAGATGCTGTATGCAGAGGACACACAGTGGATT 457
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1669 TGAACGAGCTCCCTTTCAAGATAAAAGAGGAGCACTTCAATCGGCTTAGACACTCTCTA 1728
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```
VERSION      AW160234.1  GI:6279768
KEYWORDS
SOURCE       Lycopersicon pennellii.
ORGANISM     Lycopersicon pennellii.

REFERENCE
AUTHORS      Alcalá,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.,
              Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii,
              ,C.Y., Bowman,C.I., Nierman,W., Fraser,C.M., Venter,J.C., Martin
              ,G.B., Tanksley,S.D. and Giovannoni,J.
              Generation of ESTs from wild tomato (Lycopersicon pennellii)
              trichomes
              Unpublished (1999)
JOURNAL      Contact: CUGI
COMMENT      Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Email: http://www.genome.clemson.edu/orders/index.html
              5 prime sequence.
              Location/Qualifiers
FEATURES     source
              1..557
               /organism="Lycopersicon pennellii"
               /db_xref="taxon:28526"
               /clone="cLPT19"
               /clone_lib="L.pennellii trichome, Cornell University"
               /tissue_type="trichome"
               /dev_stage="mixed stages"
               /lab_host="SOLR"
               /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
               xhoI; Leaves of various stages were shaken in liquid
               nitrogen, shearing off trichomes. This procedure yielded a
               mixture of cells highly enriched for trichomes, with minor
               contamination by other types of leaf cells."
BASE COUNT   137 a 120 c 128 g 172 t
ORIGIN
Query Match      11.5%; Score 249; DB 9; Length 557;
Best Local Similarity 77.1%; Pred. No. 1.4e-44;
Matches 334; Conservative 0; Mismatches 75; Indels 30; Gaps 3;

QY  247 ATAGTAGACTGCGTTTCTCGATTGCAATGACATGACGCGGAAGCAGTAGTAGTATGCTGCA 306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  129 ATAGTAGAAGCTGTTTTCGGATTCCAATGATATTAGTGAAGCAGTAGTAGTATGCTGCA 188
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  307 TCGCGCGCGCATGACTGTAATTTTCTCGCGGAGACTTCGCGCGGAGAGATCACTTCAC 366
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  189 TGAACGAAT-----CGGAAACTTCACGGCAGACGTCATTCCTCC 227
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  367 TGAACCCCTATCGGAACACTGGAATCTATCTTCGATGCGTCTTTGCCGGAGTTTGACT 426
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  228 TCAACGCTATCAGAAACACTAGAGCTATCTTCGATGCGTCTGCGCGGATTCGACT 287
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  427 ACTTCGCCGACGCTAAGCTTTGTGTTTCGGGCCCGGTGTAAGAAATTCGGGTGCACCGGT 486
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  288 TCITTCGTGATGCGAAGCTTCTGGCTCCAGGC---GGAAGGAAATTCGGGTGCACCGGT 344
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  487 GCATTTTGTGCGGAGAGTCCGTTCTTTAAGAAATTTGTTCTCGGTTAAAGGAGAAGA 546
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  345 GCATTTTGTGCGGAGAGTCCCTTTTAAAGAAATTTGTTCTCGGTTAAAGGAGAAGA 398
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  547 ATAGTAGAGTGGAAATCAAGGAGGTGATGAAAGAGCATGAGGTGAGCTATGAGCTG 606
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  399 GCAACAGAGCTGGAACTCAAGAGCTGATGAAAGAGTATGAGGTGAGTTTATGCGG 458
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  607 TAATGAGTGTATGGCTTATTGTATAGTGGTAAAGTTAGGCCCTTCCACCTAAGATGTGT 666
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  459 TGGTCAGTGTGCTGCGCTATTGTATAGTGGAAAGTTAGGCCCTGTCATCTAAGAGATGTGT 518
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  667 GTGTTTGTGGAGACATGACTGCTCTCATGTGCGTTGTA 705
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db  519 GTGTTTGTGTCGACAATGAGTGTTCATGATGAGTTGTA 557

RESULT 9
AV551266
LOCUS     AV551266 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
DEFINITION
          CDNA clone RZ123e05R 5', mRNA sequence.
ACCESSION AV551266
VERSION   AV551266.1 GI:8722679
KEYWORDS  EST.
SOURCE    thale cress.
          Arabidopsis thaliana
          Arabidopsi
REFERENCE 1 (bases 1 to 573)
AUTHORS   Asamizu,B., Nakamura,Y., Sato,S. and Tabata,S.
TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
          of 12,028 non-redundant expressed sequence tags from normalized and
          size-selected cDNA libraries
JOURNAL   DNA Res. 7, 175-180 (2000)
MEDLINE   20363093
COMMENT   Contact: Erika Asamizu
          The First Laboratory for Plant Gene Research
          Kazusa DNA Research Institute
          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
          Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES  source
          1..573
           /organism="Arabidopsis thaliana"
           /strain="Columbia"
           /db_xref="taxon:3702"
           /clone="RZ123e05R"
           /clone_lib="Arabidopsis thaliana roots Columbia"
           /tissue_type="roots"
           /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
           xhoI"
BASE COUNT 181 a 104 c 137 g 151 t
ORIGIN
Query Match      10.8%; Score 234.2; DB 9; Length 573;
Best Local Similarity 64.1%; Pred. No. 2.6e-41;
Matches 375; Conservative 0; Mismatches 198; Indels 12; Gaps 1;

QY  907 TCAAGTCTAATGTTGATATATAACCCCTTGATAAGCCCTTGCCCTCATGACATTTGTAAC 966
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 TCAAGTCTAATGTTAGATATGTTAGTCTTGAAAAGTCATTGCCGGAAGAGCTTGTAAAG 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  967 AAATTACTGATTCAGGACGGCAACTTGGTCTACAGGGCCCTGAAAGCAACGGTTTTCCTG 1026
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  61 AGATAAATGATAGACGTAAAGAGCTTGGTTTGGAGGTACCTAAAGATAAG----- 110
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  1027 ATAAACATGTTAAGAGGATACATAGGCGATTGGGATTCGTGATGATGTTGAATTACTACAAA 1086
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  111 --AAACATGTCGATGTACATAGGCACTTGACTCGGATGATATTGAGTTAGTCAAGT 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  1087 TGTTCCTAAGAGAGGGGCATACCTACCCCTAGATGATGATATGCTCTCCATTTATGCTGTAG 1146
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  169 TGCTTTTGAAGAGGATCACACCAATCTAGATGATGCTGTGCTCTTCATTTCCGCTGTG 228
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  1147 CGTATTTGGGATGCAAGACTACAGGAGAACTCTAGATCTTTCGACTTCCTCATATTAATC 1206
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  229 CATATTGCAATGTGAAGACCCGACACAGATCTTTTAAACTTGTATCTTCCCATGTCACAC 288
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  1207 ATCAAAATTCAGGGGATACAGGTGCTGATGTTGCGAGCCATGAGGAAAGAGCCTAAAA 1266
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  289 ATAGGAATCCGAGGGGATATACCGTCTCTCATGTTGCTGCCATCGGAGGAGCCACAAT 348
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  1267 TTGTAGTGTCCCTTTTAAACCAAGAGGAGTAGACCTTCTGATCTGCATCCGATCGAAGAA 1326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  349 TGATACTACTCTCTATTGGAAAAAGGTGCAAGTGTCATCAGAAGCAACTTTTGAAGGTAGAA 408
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```

QY 1327 AAGCACTTCAAAATCGCGAAGAGCGCTCACTAGGCTTGTGGATTTCAGTAAGTCTCCGGAGG 1386
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 409 CCGCACTCATGATCGGAAACAAGCACTATGCGCGTTGAATGTAATATATCCCGGAGC 468
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1387 AAGGAAAATCTGCTTCCGAATGATCGGTTATGCAATTCAGATTCTGGAGCAGCAGAAAGAA 1446
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 469 AATGCAAGCAATCTCTCAAGGCGGCACTATGTGTAGAAATACTAGAGCAAGAAGACAAAC 528
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1447 GAGACCCCTCTGCTAGGAGAGCTTCTGTATCTTCTTCTGCTATGCGAG 1491
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 529 GAGAACAAATTCCTAGAGATGTTCTCTCCCTCTTTTTCAGTGGCGG 573
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
BE493178          455 bp  mRNA  linear  EST 16-APR-2001
LOCUS             WHE0570_C11_F22E Triticum monococcum vegetative apex cDNA library
DEFINITION        Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
ACCESSION         BE493178
VERSION           BE493178.1  GI:9659771
SOURCE            Triticum monococcum.
ORGANISM          Triticum monococcum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 455)
Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
Stamova,B. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Vegetative apex cDNA library from Triticum monococcum
Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene T3 primer.

FEATURES             source
    Location/Qualifiers
        1..455
            /organism="Triticum monococcum"
            /cultivar="DV92"
            /db_xref="taxon:4568"
            /clone_lib="WHE0570_C11_F22"
            /clone="WHE0570_C11_F22"
            /library="
            /tissue_type="Vegetative shoot apex"
            /dev_stage="Three weeks-old plants"
            /lab_host="E. coli XL0LR"
            /note="Vector: Lambda pBK-CMV (Lambda Zap Express),
            excised phagemid; Site_1: EcoRI; Site_2: XhoI; The tissue,
            total RNA, and poly(A) RNA were prepared, a cDNA library
            was made, and the cDNA clones were in vivo excised at the
            University of California, Davis (V. Echenique, B. Stamova
            , J. Dubcovsky). Plasmid DNA preparations and DNA
            sequencing were performed in the OD Anderson lab (all
            other authors)."
```

```

BASE COUNT          132 a  94 c  98 g  131 t
ORIGIN
Query Match          10.7%; Score 232; DB 10; Length 455;
Best Local Similarity 69.9%; Pred. No. 8.1e-41;
Matches 313; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 833 GATGGTTTATCTGTTGCAACATTTGGTAAAGCATGCGAGAGATTGCTTCAAGCTG 892
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8 GTTGATCTATCTGTGCAACATTTATGCAACAAATCTTGGCGTGAACCTGTTGAGAGATG 97
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

QY 893 CATTGAGATTATTGTCAAGTCTAATGTTGATATACATACCCTTGATAAAGCCTTTCCTCA 952
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 CTGGAGATGGTAGTCCCGCTCAATCTTGACATGATGTTACTCTTGAGAAAGCATTTGCCCTGA 127
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 953 TGACATTTGAAACAAATTTACTGATTACGAGCGGAACTTGTGCTACAAAGGCGCTGAAG 1012
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 AGATGTTATCAAGCAAAATTTATTGATTACCGGATAACTCTTGGATTAGCTTCACCCGAAGA 187
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1013 CAACGGTTTCTGTATAAACATGTTAAGAGGATACATAGGCGCATTTGGATCTGATGATG 1072
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 188 CAATGGCTGTCTCTACAAACACGTAAGAAGGATACTCAAGGCACCTTGATCTGATGATGT 247
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1073 TGAATTACTACAAATGTTCTTAAGAGAGGGGCATACCTACCTAGATGATGATATGTCTCT 1132
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 248 GGAGCTTGTCAAGGATGCTGCTCACAGAAGGCGACACTAACCTTGATGATGATTTGCAATT 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1133 CAATTATGCTGTAGGATTAATTCGGATGCAAGACTACAGCAAACTTCTAGATTTGCACT 1192
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 308 GCACATGCTGTAGAACACTGTGACTCAAAAATTACAACAGAACTTCTGGACATCGCACT 367
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1193 TGCTCATATTAAATCATCAAAATTTCAAGGGGATACACGGTGTGTCATGTTGCAGCCATGAG 1252
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 368 TCGGATGTTAATCTCAGAAACCCCAAGAGTTATACTGTTCTTCACATCCGCTGTAGGCG 427
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1253 GAAAGAGCCTAAATTTAGTGTCCCTT 1280
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 428 GAGAGATCCTAAATTTGTTGTTCCCTT 455
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 11
BH525927/c       772 bp  DNA  linear  GSS 13-DEC-2001
LOCUS             BOGT004TF BOGT Brassica oleracea genomic clone BOGT004, DNA
DEFINITION        BH525927
ACCESSION         BH525927
VERSION           BH525927.1  GI:17734012
KEYWORDS          GSS.
SOURCE            Brassica oleracea.
ORGANISM          Brassica oleracea.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 772)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOGT004TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

```

```

FEATURES             source
    Location/Qualifiers
        1..772
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
            /db_xref="taxon:3712"
            /clone="BOGT004"
            /clone_lib="BOGT"
            /note="Vector: pBstXI; Site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pBstXI using BstXI linkers"
```

```

BASE COUNT          199 a  187 c  176 g  210 t
ORIGIN
Query Match          9.7%; Score 211.2; DB 12; Length 772;
Best Local Similarity 61.0%; Pred. No. 3.1e-36;
Matches 367; Conservative 0; Mismatches 223; Indels 12; Gaps 1;

QY 934 TTGATAAGCCTTGCCTCATGACATTTGTAACAAATTAATGATTACGAGCGGAACCTTG 993
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```
Query Match      8.3%; Score 179.6; DB 9; Length 458;
Best Local Similarity 62.8%; Pred. No. 3e-29;
Matches 278; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 1036 TTAAGAGGATACATAGGCGATTTGGATTCGTGATGATGTTGAATTACTACAAATGTTGCTAA 1095
DB 7 TCACATAGATACACAGGCAATTTGGATTCAGATGATGTTGAGCTTGTAAACTTCTTTTAA 66

QY 1096 GAGAGGGGCACTACTACCCCTAGATGATGATGATGCTCTCCATTTATGCTGTAGGCTATTGCG 1155
DB 67 ATGAATCAGACATTAATCTTAGATGAAGCAATGCTCTCCATTTATGCTGTAGGCTATTGCG 126

QY 1156 ATGCAAGGACTACAGCAGAACTTCTAGATCTTTCGACTTTCGCTGATATTAATCATCAAAAT 1215
DB 127 ATCCCAAGGTGTTCTGAGGTACTTGGTTTGGGACTCGCTAATGCTCAATCTTCGAAAT 186

QY 1216 CAAGGGGATACAGGGTGTGATGTTTGCAGCCATGAGAAAGAGCTTAAATTTAGTGT 1275
DB 187 CTAGGGGGTACACAGTGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246

QY 1276 CCCTTTTAAACCAAGGAGCTAGACCTTCTGATCTGATCTGATCCGATGGAAGAAAGCACTTC 1335
DB 247 CCCTACTTACGAAGGGGCTTGTGCATCAGATTTGACCTTTTGTGCTGCTGCTGCTGCTGCT 306

QY 1336 AAATGCCAAGAGGCTCACTAGGCTTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1395
DB 307 GTATTTGTAGGAGTTGACAGGCCAAGCAAGATTTATCATGCAAAACAGAGCANGGAAAG 366

QY 1396 CTGCTTCGAATGATCGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1455
DB 367 AAACAAACCAAGATCGGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 426

QY 1456 TGCTAGGAGAAGCTTCTGTATCT 1478
DB 427 TGCTTTGGGATGCTGTATGCT 449

RESULT 15
AW399343
LOCUS
DEFINITION
EST309843 L. pennellii trichome, Cornell University Lycopersicon
pennellii cDNA clone cLPT7013 5', mRNA sequence.
ACCESSION
VERSION
AW399343.1 GI:6917813
KEYWORDS
SOURCE
EST.
ORGANISM
Lycopersicon pennellii.
Lycopersicon pennellii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 450)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.,
Liang,F., Hansen,T.S., Opton,J., Ronning,C.M., Craven,M.B., Fujii
,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
trichomes
JOURNAL
Unpublished (1999)
COMMENT
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Location/Qualifiers
Source
1..450
/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT7013"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
```

Search completed: October 8, 2002, 01:20:39
Job time : 1710.05 secs

```
/lab_host="SOLR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
BASE COUNT      120 a      85 c      116 g      129 t
ORIGIN

Query Match      7.9%; Score 171.8; DB 9; Length 450;
Best Local Similarity 61.5%; Pred. No. 1.6e-27;
Matches 275; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 1041 AGGATACATAGGGGATTTGGATTTCTGATGATGTTGAATTACTACAAATGTTGCTAAGAGAG 1100
DB 2 AGGATATACAGGCAATTTGGATTCGGATGATGTTGAACCTTTGCAAGCTTTTACTTAATGAG 61

QY 1101 GGGCATCTACCCCTAGATGATGATGATGCTCTCCATTTATGCTGTAGGCTATTGCGATGCA 1160
DB 62 TCTGACATAAGTTTAGATGGAGCCTACGCTTTCATTTACGCTGTTGCTATTTGTGACCCC 121

QY 1161 AAGACTACAGCAGAACTTCTAGATCTTGCACCTTCTGATATTAATCATCAAAATTTCAAGG 1220
DB 122 AAGGTTGTTGCTGAGGTTCTTTGGACTGGGTGCTTAATGTCACCTTCGGAATGCACGT 181

QY 1221 GGATACACGGTGTGCTGATGTTTGCAGCCATGAGGAAAGAGCCTAAATTTGTAGTCCCTTT 1280
DB 182 GGTACACTGTGCTTCACATTTGCTGCCATCGTAAGCAACCTTCATTTGATCACTT 241

QY 1281 TTAACCAAGAGGTAGACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAATC 1340
DB 242 TTAACCAAGAGGTAGACCTTCTGATCTGACATCCGATGGAAGAAAGCACTTCAATC 301

QY 1341 GCCAAGAGGCTCACTAGGCTTGTGATTTTCCAGTAAGTCTCCGGAGGAAGAAATCTGCT 1400
DB 302 TGTAGGAGGCTGACTAGGCTTAAGAGTACCATGCCAAAACAGACAGAGGCGAGGAAGCA 361

QY 1401 TCGAATGATCGGTTTATGATTTGATTTCTGAGCAAGCAGAAAGAGAGACCCCTCTGCTA 1460
DB 362 AACAAAGATCGGATGATGATTTGATGATTTTGGAGAGAGAGATGCGTCGCAACCAATGACC 421

QY 1461 GGAGAAGCTTCTGATCTCTTGTCTATG 1487
DB 422 GGAGATGCATTTATTTCTTGTGCCCATG 448

Search completed: October 8, 2002, 01:20:39
Job time : 1710.05 secs
```